

#3

<110> U.S. Army Medical Research & Material Command

<120> RECOMBINANT VACCINE AGAINST BOTULINUM  
NEUROTOXIN

<130> A33626-A 067252.0107

<150> PCT/NS00/12890  
<151> 2000-05-12

<150> 09/611,419  
<151> 2000-07-06

<150> 60/133,865  
<151> 1999-05-12

<150> 60/133,866  
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<150> 60/133,873  
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<150> 08/123,975  
<151> 1993-09-21

<160> 34

<170> FastSEQ for Windows Version 4.0

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<211> 1332  
<212> DNA  
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<220>  
<223> Synthetic construct based on Clostridium botulinum  
sequence

<221> CDS  
<222> (13) ... (1326)

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Met Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn  
1 5 10

atc atc aat acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu	15	20	25	99
atc gac ctg tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val	30	35	40	45
aac ttc gat ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu	50	55	60	195
tct tcc aaa atc gaa gtt atc ctg aag aat gct atc gta tac aac tct Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser	65	70	75	243
atg tac gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr	80	85	90	291
ttc aac tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met	95	100	105	339
gaa aac aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile	110	115	120	125
tgg act ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys	130	135	140	387
tac tct cag atg atc aac atc tct gac tac atc aat cgc tgg atc ttc Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe	145	150	155	435
gtt acc atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn	160	165	170	483
ggc cgt ctg atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His	175	180	185	531
gct tct aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His	190	195	200	579
cgc tac atc tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn	210	215	220	627
gaa aaa gaa atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile	225	230	235	675
ctg aaa gac ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac				723

Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr			
240	245	250	
atg ctg aat ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta			819
Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val			
255	260	265	
ggt atc cgc ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg			867
Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met			
270	275	280	285
act acc aac atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc			915
Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe			
290	295	300	
atc atc aag aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac			963
Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn			
305	310	315	
aat gat cgt gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt			1011
Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg			
320	325	330	
ctg gct acc aat gct tct cag gct ggt gta gaa aag atc ttg tct gct			1059
Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala			
335	340	345	
ctg gaa atc ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa			1107
Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys			
350	355	360	365
tcc aag aac gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag			1155
Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln			
370	375	380	
gac aac aat ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac			1203
Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn			
385	390	395	
aat atc gct aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa			1251
Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu			
400	405	410	
cgt tcc tct cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat			1299
Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp			
415	420	425	
gac ggt tgg ggt gaa cgt ccg ctg taa gaattc			1332
Asp Gly Trp Gly Glu Arg Pro Leu *			
430	435		

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<210> 2
<211> 437
<212> PRT
<213> Artificial Sequence
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<220>

<223> Synthetic construct based on Clostridium botulinum  
sequence

<400> 2

Met Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn  
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Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu  
20 25 30  
Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp  
35 40 45  
Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys  
50 55 60  
Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu  
65 70 75 80  
Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser  
85 90 95  
Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn  
100 105 110  
Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu  
115 120 125  
Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln  
130 135 140  
Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile  
145 150 155 160  
Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu  
165 170 175  
Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn  
180 185 190  
Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile  
195 200 205  
Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu  
210 215 220  
Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp  
225 230 235 240  
Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn  
245 250 255  
Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg  
260 265 270  
Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn  
275 280 285  
Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys  
290 295 300  
Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg  
305 310 315 320  
Val Tyr Ile Asn Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr  
325 330 335  
Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile  
340 345 350  
Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn  
355 360 365  
Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn  
370 375 380  
Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala  
385 390 395 400  
Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser

405 410 415  
Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp  
420 425 430  
Gly Glu Arg Pro Leu  
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<210> 3  
<211> 1323  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic construct based on Clostridium botulinum  
sequence

<221> CDS  
<222> (13)...(1314)  
<223> Synthetic Construct

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Met Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn  
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acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg atc gac ctg 99  
Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu  
15 20 25

tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt aac ttc gat 147  
Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp  
30 35 40 45

ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa tct tcc aaa 195  
Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys  
50 55 60

atc gaa gtt atc ctg aag aat gct atc gta tac aac tct atg tac gaa 243  
Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu  
65 70 75

aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac ttc aac tcc 291  
Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser  
80 85 90

atc tct ctg aac aat gaa tac acc atc atc aac tgc atg gaa aac aat 339  
Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn  
95 100 105

tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc tgg act ctg 387  
Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu  
110 115 120 125

cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa tac tct cag 435  
Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln  
130 135 140

atg atc aac atc tct gac tac atc aat cgc tgg atc ttc gtt acc atc		483
Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile		
145	150	155
acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac ggc cgt ctg		531
Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu		
160	165	170
atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac gct tct aat		579
Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn		
175	180	185
aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac cgc tac atc		627
Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile		
190	195	200
205		
tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac gaa aaa gaa		675
Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu		
210	215	220
atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc ctg aaa gac		723
Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp		
225	230	235
ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac atg ctg aat		771
Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn		
240	245	250
ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta ggt atc cgc		819
Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg		
255	260	265
ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg act acc aac		867
Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn		
270	275	280
285		
atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc atc atc aag		915
Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys		
290	295	300
aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac aat gat cgt		963
Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg		
305	310	315
gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt ctg gct acc		1011
Val Tyr Ile Asn Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr		
320	325	330
aat gct tct cag gct ggt gta gaa aag atc ttg tct gct ctg gaa atc		1059
Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile		
335	340	345
ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa tcc aag aac		1107
Pro Asp Val Gly Asn Leu Ser Gln Val Val Met Lys Ser Lys Asn		
350	355	360
365		

gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag gac aac aat		1155
Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn		
370	375	380
ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac aat atc gct		1203
Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala		
385	390	395
aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa cgt tcc tct		1251
Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser		
400	405	410
cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat gac ggt tgg		1299
Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp		
415	420	425
ggt gaa cgt ccg ctg taagaattc		1323
Gly Glu Arg Pro Leu		
430		

<210> 4  
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<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic construct based on Clostridium botulinum  
sequence

<400> 4			
Met Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile			
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Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr			
20	25	30	
Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp			
35	40	45	
Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val			
50	55	60	
Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser			
65	70	75	80
Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu			
85	90	95	
Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp			
100	105	110	
Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr			
115	120	125	
Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn			
130	135	140	
Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn			
145	150	155	160
Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln			
165	170	175	
Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met			
180	185	190	
Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys			

195	200	205
Tyr Phe Asn Leu Phe Asp Lys Glu	Leu Asn Glu Lys Glu Ile Lys Asp	
210	215	220
Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile	Leu Lys Asp Phe Trp Gly	
225	230	235
Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr	Tyr Met Leu Asn Leu Tyr Asp	
245	250	255
Pro Asn Lys Tyr Val Asp Val Asn Asn Val	Gly Ile Arg Gly Tyr Met	
260	265	270
Tyr Leu Lys Gly Pro Arg Gly Ser Val	Met Thr Thr Asn Ile Tyr Leu	
275	280	285
Asn Ser Ser Leu Tyr Arg Gly Thr Lys	Phe Ile Ile Lys Lys Tyr Ala	
290	295	300
Ser Gly Asn Lys Asp Asn Ile Val Arg Asn	Asn Asp Arg Val Tyr Ile	
305	310	315
Asn Val Val Val Lys Asn Lys Glu	Tyr Arg Leu Ala Thr Asn Ala Ser	
325	330	335
Gln Ala Gly Val Glu Lys Ile	Leu Ser Ala Leu Glu Ile Pro Asp Val	
340	345	350
Gly Asn Leu Ser Gln Val Val Val Met	Lys Ser Lys Asn Asp Gln Gly	
355	360	365
Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp	Asn Asn Gly Asn Asp	
370	375	380
Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn	Ile Ala Lys Leu Val	
385	390	395
Ala Ser Asn Trp Tyr Asn Arg Gln Ile	Glu Arg Ser Ser Arg Thr Leu	
405	410	415
Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp	Gly Trp Gly Glu Arg	
420	425	430
Pro Leu		

<210> 5  
 <211> 1326  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic construct based on Clostridium botulinum  
 sequence

<220>  
 <221> CDS  
 <222> (13)...(1317)

<400> 5  
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 Met Ala Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile  
 1 5 10

aat acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg atc gac 99  
 Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp  
 15 20 25

ctg tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt aac ttc		147
Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe		
30	35	40
45		
gat ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa tct tcc		195
Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser		
50	55	60
aaa atc gaa gtt atc ctg aag aat gct atc gta tac aac tct atg tac		243
Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr		
65	70	75
gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac ttc aac		291
Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn		
80	85	90
tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg gaa aac		339
Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn		
95	100	105
aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc tgg act		387
Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr		
110	115	120
125		
ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa tac tct		435
Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser		
130	135	140
cag atg atc aac atc tct gac tac atc aat cgc tgg atc ttc gtt acc		483
Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr		
145	150	155
atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac ggc cgt		531
Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg		
160	165	170
ctg atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac gct tct		579
Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser		
175	180	185
aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac cgc tac		627
Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr		
190	195	200
205		
atc tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac gaa aaa		675
Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys		
210	215	220
gaa atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc ctg aaa		723
Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys		
225	230	235
gac ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac atg ctg		771
Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu		
240	245	250
aat ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta ggt atc		819

Asn	Leu	Tyr	Asp	Pro	Asn	Lys	Tyr	Val	Asp	Val	Asn	Asn	Val	Gly	Ile	
255				260					265							
cgc	ggt	tac	atg	tac	ctg	aaa	ggt	ccg	cgt	ggt	tct	gtt	atg	act	acc	867
Arg	Gly	Tyr	Met	Tyr	Leu	Lys	Gly	Pro	Arg	Gly	Ser	Val	Met	Thr	Thr	
270				275					280				285			
aac	atc	tac	ctg	aac	tct	tcc	ctg	tac	cgt	ggt	acc	aaa	ttc	atc	atc	915
Asn	Ile	Tyr	Leu	Asn	Ser	Ser	Leu	Tyr	Arg	Gly	Thr	Lys	Phe	Ile	Ile	
				290					295				300			
aag	aaa	tac	gcg	tct	ggt	aac	aag	gac	aat	atc	gtt	ccg	aac	aat	gat	963
Lys	Lys	Tyr	Ala	Ser	Gly	Asn	Lys	Asp	Asn	Ile	Val	Arg	Asn	Asn	Asp	
				305					310				315			
cgt	gta	tac	atc	aat	gtt	gta	gtt	aag	aac	aaa	gaa	tac	cgt	ctg	gct	1011
Arg	Val	Tyr	Ile	Asn	Val	Val	Val	Lys	Asn	Lys	Glu	Tyr	Arg	Leu	Ala	
				320					325				330			
acc	aat	gct	tct	cag	gct	ggt	gta	gaa	aag	atc	ttg	tct	gct	ctg	gaa	1059
Thr	Asn	Ala	Ser	Gln	Ala	Gly	Val	Glu	Lys	Ile	Leu	Ser	Ala	Leu	Glu	
				335					340				345			
atc	ccg	gac	gtt	ggt	aat	ctg	tct	cag	gta	gtt	atg	aaa	tcc	aag		1107
Ile	Pro	Asp	Val	Gly	Asn	Leu	Ser	Gln	Val	Val	Val	Met	Lys	Ser	Lys	
				350					355				360			365
aac	gac	cag	ggt	atc	act	aac	aaa	tgc	aaa	atg	aat	ctg	cag	gac	aac	1155
Asn	Asp	Gln	Gly	Ile	Thr	Asn	Lys	Cys	Lys	Met	Asn	Leu	Gln	Asp	Asn	
				370					375				380			
aat	ggt	aac	gat	atc	ggt	ttc	atc	ggt	ttc	cac	cag	ttc	aac	aat	atc	1203
Asn	Gly	Asn	Asp	Ile	Gly	Phe	Ile	Gly	Phe	His	Gln	Phe	Asn	Asn	Ile	
				385					390				395			
gct	aaa	ctg	gtt	gct	tcc	aac	tgg	tac	aat	cgt	cag	atc	gaa	cgt	tcc	1251
Ala	Lys	Leu	Val	Ala	Ser	Asn	Trp	Tyr	Asn	Arg	Gln	Ile	Glu	Arg	Ser	
				400					405				410			
tct	ccg	act	ctg	ggt	tgc	tct	tgg	gag	ttc	atc	ccg	gtt	gat	gac	ggt	1299
Ser	Arg	Thr	Leu	Gly	Cys	Ser	Trp	Glu	Phe	Ile	Pro	Val	Asp	Asp	Gly	
				415					420				425			
tgg	ggt	gaa	cgt	ccg	ctg	taagaattc										1326
Trp	Gly	Glu	Arg	Pro	Leu											
				430					435							

<210> 6  
<211> 435  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic construct based on Clostridium botulinum  
sequence

<400> 6

Met Ala Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser  
1 5 10 15  
Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg  
20 25 30  
Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile  
35 40 45  
Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu  
50 55 60  
Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe  
65 70 75 80  
Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser  
85 90 95  
Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly  
100 105 110  
Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp  
115 120 125  
Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile  
130 135 140  
Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn  
145 150 155 160  
Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp  
165 170 175  
Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile  
180 185 190  
Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile  
195 200 205  
Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys  
210 215 220  
Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp  
225 230 235 240  
Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr  
245 250 255  
Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr  
260 265 270  
Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr  
275 280 285  
Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr  
290 295 300  
Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr  
305 310 315 320  
Ile Asn Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala  
325 330 335  
Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp  
340 345 350  
Val Gly Asn Leu Ser Gln Val Val Met Lys Ser Lys Asn Asp Gln  
355 360 365  
Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn  
370 375 380  
Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu  
385 390 395 400  
Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr  
405 410 415  
Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu  
420 425 430  
Arg Pro Leu

<210> 7  
 <211> 1341  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic construct based on Clostridium botulinum sequence

<221> CDS  
 <222> (10) ... (1329)

<400> 7  
 gaattcacg atg gcc aac aaa tac aat tcc gaa atc ctg aac aat atc atc 51  
 Met Ala Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile  
 1 5 10

ctg aac ctg cgt tac aaa gac aac aat ctg atc gat ctg tct ggt tac 99  
 Leu Asn Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr  
 15 20 25 30

ggt gct aaa gtt gaa gta tac gac ggt gtt gaa ctg aat gac aag aac 147  
 Gly Ala Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn  
 35 40 45

cag ttc aaa ctg acc tct tcc gct aac tct aag atc cgt gtt act cag 195  
 Gln Phe Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln  
 50 55 60

aat cag aac atc atc ttc aac tcc gta ttc ctg gac ttc tct gtt tcc 243  
 Asn Gln Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser  
 65 70 75

ttc tgg att cgt atc ccg aaa tac aag aac gac ggt atc cag aat tac 291  
 Phe Trp Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr  
 80 85 90

atc cac aat gaa tac acc atc atc aac tgc atg aag aat aac tct ggt 339  
 Ile His Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly  
 95 100 105 110

tgg aag atc tcc atc cgc ggt aac cgt atc atc tgg act ctg atc gat 387  
 Trp Lys Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp  
 115 120 125

atc aac ggt aag acc aaa tct gta ttc ttc gaa tac aac atc cgt gaa 435  
 Ile Asn Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu  
 130 135 140

gac atc tct gaa tac atc aat cgc tgg ttc ttc gtt acc atc acc aat 483  
 Asp Ile Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn  
 145 150 155

aac ctg aac aat gct aaa atc tac atc aac ggt aaa ctg gaa tct aat		531	
Asn Leu Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn			
160	165	170	
acc gac atc aaa gac atc cgt gaa gtt atc gct aac ggt gaa atc atc		579	
Thr Asp Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile			
175	180	185	190
ttc aaa ctg gac ggt gac atc gat cgt acc cag ttc atc tgg atg aaa		627	
Phe Lys Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys			
195	200	205	
tac ttc tcc atc ttc aac acc gaa ctg tct cag tcc aat atc gaa gaa		675	
Tyr Phe Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu			
210	215	220	
cgg tac aag atc cag tct tac tcc gaa tac ctg aaa gac ttc tgg ggt		723	
Arg Tyr Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly			
225	230	235	
aat ccg ctg atg tac aac aaa gaa tac tat atg ttc aat gct ggt aac		771	
Asn Pro Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn			
240	245	250	
aag aac tct tac atc aaa ctg aag aaa gac tct ccg gtt ggt gaa atc		819	
Lys Asn Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile			
255	260	265	270
ctg act cgt tcc aaa tac aac cag aac tct aaa tac atc aac tac cgc		867	
Leu Thr Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg			
275	280	285	
gac ctg tac atc ggt gaa aag ttc atc atc cgt cgc aaa tct aac tct		915	
Asp Leu Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser			
290	295	300	
cag tcc atc aat gat gac atc gta cgt aaa gaa gac tac atc tac ctg		963	
Gln Ser Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu			
305	310	315	
gac ttc ttc aac ctg aat cag gaa tgg cgt gta tac acc tac aag tac		1011	
Asp Phe Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr			
320	325	330	
ttc aag aaa gaa gaa aag ctt ttc ctg gct ccg atc tct gat tcc		1059	
Phe Lys Lys Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser			
335	340	345	350
gac gaa ctc tac aac acc atc cag atc aaa gaa tac gac gaa cag ccg		1107	
Asp Glu Leu Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro			
355	360	365	
acc tac tct tgc cag ctg ttc aag aaa gat gaa gaa tct act gac		1155	
Thr Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp			
370	375	380	
gaa atc ggt ctg atc ggt atc cac cgt ttc tac gaa tct ggt atc gta		1203	

Glu Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile Val			
385	390	395	
ttc gaa gaa tac aaa gac tac ttc tgc atc tcc aaa tgg tac ctg aag 1251			
Phe Glu Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys			
400	405	410	
gaa gtt aaa cgc aaa ccg tac aac ctg aaa ctg ggt tgc aat tgg cag 1299			
Glu Val Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln			
415	420	425	430
ttc atc ccg aaa gac gaa ggt tgg acc gaa tagtaagaat tc 1341			
Phe Ile Pro Lys Asp Glu Gly Trp Thr Glu			
435	440		
<210> 8			
<211> 440			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> Synthetic construct based on Clostridium botulinum sequence			
<400> 8			
Met Ala Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn			
1	5	10	15
Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala			
20	25	30	
Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn Gln Phe			
35	40	45	
Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln Asn Gln			
50	55	60	
Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser Phe Trp			
65	70	75	80
Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr Ile His			
85	90	95	
Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly Trp Lys			
100	105	110	
Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Ile Asn			
115	120	125	
Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu Asp Ile			
130	135	140	
Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn Asn Leu			
145	150	155	160
Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn Thr Asp			
165	170	175	
Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile Phe Lys			
180	185	190	
Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe			
195	200	205	
Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu Arg Tyr			
210	215	220	
Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro			
225	230	235	240

Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn  
     245                     250                     255  
 Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile Leu Thr  
     260                     265                     270  
 Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg Asp Leu  
     275                     280                     285  
 Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser  
     290                     295                     300  
 Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu Asp Phe  
     305                     310                     315                     320  
 Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr Phe Lys  
     325                     330                     335  
 Lys Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser Asp Glu  
     340                     345                     350  
 Leu Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro Thr Tyr  
     355                     360                     365  
 Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp Glu Ile  
     370                     375                     380  
 Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile Val Phe Glu  
     385                     390                     395                     400  
 Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val  
     405                     410                     415  
 Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile  
     420                     425                     430  
 Pro Lys Asp Glu Gly Trp Thr Glu  
     435                     440

<210> 9  
 <211> 1371  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic construct based on Clostridium botulinum  
 sequence  
 <221> CDS  
 <222> (10) ... (1359)

<400> 9  
 gaattcacg atg acc atc cca ttc aac atc ttc tcc tac acc aac aac tcc 51  
 Met Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser  
     1                     5                     10

ctg ttg aag gac atc atc aac gag tac ttc aac aac atc aac gac tcc 99  
 Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile Asn Asp Ser  
     15                     20                     25                     30

aag atc ctg tcc ctg cag aac cgt aag aac acc ttg gtc gac acc tcc 147  
 Lys Ile Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val Asp Thr Ser  
     35                     40                     45

ggt tac aac gcc gag gtc tcc gag gag ggt gac gtc cag ctg aac cca 195  
 Gly Tyr Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln Leu Asn Pro  
     50                     55                     60

atc ttc cca ttc gac ttc aag ctg ggt tcc tcc ggt gag gac aga ggt Ile Phe Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu Asp Arg Gly	65	70	75	243
aag gtc atc gtc acc cag aac gag aac atc gtc tac aac tcc atg tac Lys Val Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn Ser Met Tyr	80	85	90	291
gag tcc ttc tcc atc tcc ttc tgg atc aga atc aac aag tgg gtc tcc Glu Ser Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys Trp Val Ser	95	100	105	339
aac ttg cca ggt tac acc atc atc gac tcc gtc aag aac aac tcc ggt Asn Leu Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn Asn Ser Gly	115	120	125	387
tgg tcc atc ggt atc atc tcc aac ttc ctg gtc ttc acc ctg aag cag Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr Leu Lys Gln	130	135	140	435
aac gag gac tcc gag cag tcc atc aac ttc tcc tac gac atc tcc aac Asn Glu Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp Ile Ser Asn	145	150	155	483
aac gct cct ggt tac aac aag tgg ttc ttc gtc acc gtc acc aac aac Asn Ala Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val Thr Asn Asn	160	165	170	531
atg atg ggt aac atg aag atc tac atc aac ggt aag ctg atc gac acc Met Met Gly Asn Met Lys Ile Tyr Ile Asn Gly Lys Leu Ile Asp Thr	175	180	185	579
190				
atc aag gtc aag gag ttg acc ggt atc aac ttc tcc aag acc atc acc Ile Lys Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys Thr Ile Thr	195	200	205	627
ttc gag atc aac aag atc cca gac acc ggt ctg atc acc tcc gac tcc Phe Glu Ile Asn Lys Ile Pro Asp Thr Gly Leu Ile Thr Ser Asp Ser	210	215	220	675
225				
gac aac atc aac atg tgg atc cgt gac ttc tac atc ttc gcc aag gag Asp Asn Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe Ala Lys Glu	230	235	235	723
240				
ttg gac ggt aag gac atc aac atc ctg ttc aac tcc ttg cag tac acc Leu Asp Gly Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu Gln Tyr Thr	245	250	250	771
255				
aac gtc gtc aag gac tac tgg ggt aac gac ctg aga tac aac aag gag Asn Val Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr Asn Lys Glu	260	265	270	819
275				
tac tac atg gtc aac atc gac tac ttg aac aga tac atg tac gcc aac Tyr Tyr Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met Tyr Ala Asn	280	285	285	867

tcc aga cag atc gtc ttc aac acc aga cgt aac aac gac ttc aac		915	
Ser Arg Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn Asp Phe Asn			
290	295	300	
gag ggt tac aag atc atc atc aag cgt atc aga ggt aac acc aac gac		963	
Glu Gly Tyr Lys Ile Ile Lys Arg Ile Arg Gly Asn Thr Asn Asp			
305	310	315	
acc aga gtc aga ggt ggt gac atc ctg tac ttc gac atg act atc aac		1011	
Thr Arg Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr Ile Asn			
320	325	330	
aac aag gcc tac aac ctg ttc atg aag aac gag acc atg tac gcc gac		1059	
Asn Lys Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met Tyr Ala Asp			
335	340	345	350
aac cac tcc acc gag gac atc tac gcc atc ggt ctg cgt gag cag acc		1107	
Asn His Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg Glu Gln Thr			
355	360	365	
aag gac atc aac gac aac atc atc ttc cag atc cag cca atg aac aac		1155	
Lys Asp Ile Asn Asp Asn Ile Ile Phe Gln Ile Gln Pro Met Asn Asn			
370	375	380	
act tac tac tac gct tcc cag atc ttc aag tcc aac ttc aac ggt gag		1203	
Thr Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe Asn Gly Glu			
385	390	395	
aac atc tcc ggt atc tgt tcc atc ggt acc tac aga ttc cgt ctg ggt		1251	
Asn Ile Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe Arg Leu Gly			
400	405	410	
ggt gac tgg tac aga cac aac tac ttg gtt cca act gtc aag cag ggt		1299	
Gly Asp Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val Lys Gln Gly			
415	420	425	430
aac tac gcc tcc ttg ctg gag tcc act tcc acc cac tgg gga ttc gtc		1347	
Asn Tyr Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp Gly Phe Val			
435	440	445	
cca gtc tcc gag taataggaat tc		1371	
Pro Val Ser Glu			
450			

<210> 10  
<211> 450  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic construct based on Clostridium botulinum  
sequence

<400> 10  
Met Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu

1	5	10	15
Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile Asn Asp Ser Lys Ile			
20	25	30	
Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val Asp Thr Ser Gly Tyr			
35	40	45	
Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln Leu Asn Pro Ile Phe			
50	55	60	
Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu Asp Arg Gly Lys Val			
65	70	75	80
Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn Ser Met Tyr Glu Ser			
85	90	95	
Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys Trp Val Ser Asn Leu			
100	105	110	
Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn Asn Ser Gly Trp Ser			
115	120	125	
Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr Leu Lys Gln Asn Glu			
130	135	140	
Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp Ile Ser Asn Asn Ala			
145	150	155	160
Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val Thr Asn Asn Met Met			
165	170	175	
Gly Asn Met Lys Ile Tyr Ile Asn Gly Lys Leu Ile Asp Thr Ile Lys			
180	185	190	
Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys Thr Ile Thr Phe Glu			
195	200	205	
Ile Asn Lys Ile Pro Asp Thr Gly Leu Ile Thr Ser Asp Ser Asp Asn			
210	215	220	
Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe Ala Lys Glu Leu Asp			
225	230	235	240
Gly Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu Gln Tyr Thr Asn Val			
245	250	255	
Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr Asn Lys Glu Tyr Tyr			
260	265	270	
Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met Tyr Ala Asn Ser Arg			
275	280	285	
Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn Asp Phe Asn Glu Gly			
290	295	300	
Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn Thr Asn Asp Thr Arg			
305	310	315	320
Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr Ile Asn Asn Lys			
325	330	335	
Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met Tyr Ala Asp Asn His			
340	345	350	
Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg Glu Gln Thr Lys Asp			
355	360	365	
Ile Asn Asp Asn Ile Ile Phe Gln Ile Gln Pro Met Asn Asn Thr Tyr			
370	375	380	
Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe Asn Gly Glu Asn Ile			
385	390	395	400
Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe Arg Leu Gly Gly Asp			
405	410	415	
Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val Lys Gln Gly Asn Tyr			
420	425	430	
Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp Gly Phe Val Pro Val			
435	440	445	
Ser Glu			
450			

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<210> 11
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on Clostridium botulinum
sequence

<221> CDS
<222> (10)...(1362)

<400> 11
gaattcacg atg cgt ttg aag gct aag gtc aac gag tcc ttc gag aac acc 51
Met Arg Leu Lys Ala Lys Val Asn Glu Ser Phe Glu Asn Thr
    1           5                   10

atg cca ttc aac atc ttc tcc tac acc aac aac tcc ttg ttg aag gac 99
Met Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp
    15          20                  25                   30

atc atc aac gag tac ttc aac tcc atc aac gac tcc aag atc ttg tcc 147
Ile Ile Asn Glu Tyr Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser
    35          40                  45

ttg cag aac aag aag aac gcc ttg gtc gac acc tcc ggt tac aac gcc 195
Leu Gln Asn Lys Lys Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala
    50          55                  60

gag gtc aga gtc ggt gac aac gtc cag ttg aac acc atc tac acc aac 243
Glu Val Arg Val Gly Asp Asn Val Gln Leu Asn Thr Ile Tyr Thr Asn
    65          70                  75

gac ttc aag ttg tcc tct tcc ggt gac aag atc atc gtc aac ttg aac 291
Asp Phe Lys Leu Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn
    80          85                  90

aac aac atc ttg tac tcc gcc atc tac gag aac tcc tct gtc tcc ttc 339
Asn Asn Ile Leu Tyr Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe
    95          100                 105                  110

tgg atc aag atc tcc aag gac ttg acc aac tcc cac aac gag tac acc 387
Trp Ile Lys Ile Ser Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr
    115         120                 125

atc atc aac tcc atc gag cag aac tcc ggt tgg aag ttg tgt atc cgt 435
Ile Ile Asn Ser Ile Glu Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg
    130         135                 140

aac ggt aac atc gag tgg atc ttg cag gac gtc aac cgt aag tac aag 483
Asn Gly Asn Ile Glu Trp Ile Leu Gln Asp Val Asn Arg Lys Tyr Lys
    145         150                 155

tcc ttg atc ttc gac tac tcc gag tcc ttg tcc cac acc ggt tac acc 531
Ser Leu Ile Phe Asp Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr

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160

165

170

aac aag tgg ttc gtc acc atc acc aac aac atc atg ggt tac atg 579  
 Asn Lys Trp Phe Phe Val Thr Ile Thr Asn Asn Ile Met Gly Tyr Met  
 175 180 185 190

aag ttg tac atc aac ggt gag ttg aag cag tcc cag aag atc gag gac 627  
 Lys Leu Tyr Ile Asn Gly Glu Leu Lys Gln Ser Gln Lys Ile Glu Asp  
 195 200 205

ctg gac gag gtc aag ctg gac aag acc atc gtc ttc ggt atc gac gag 675  
 Leu Asp Glu Val Lys Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu  
 210 215 220

aac atc gac gag aac cag atg ttg tgg att cgt gac ttc aac atc ttc 723  
 Asn Ile Asp Glu Asn Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe  
 225 230 235

tcc aag gag ctg tcc aac gag gac atc aac atc gtc tac gag ggt cag 771  
 Ser Lys Glu Leu Ser Asn Glu Asp Ile Asn Ile Val Tyr Glu Gly Gln  
 240 245 250

atc ctg agg aac gtc atc aag gac tac tgg ggt aac cca ctg aag ttc 819  
 Ile Leu Arg Asn Val Ile Lys Asp Tyr Trp Gly Asn Pro Leu Lys Phe  
 255 260 265 270

gac acc gag tac tac atc atc aac gac aac tac atc gac cgt tac atc 867  
 Asp Thr Glu Tyr Tyr Ile Ile Asn Asp Asn Tyr Ile Asp Arg Tyr Ile  
 275 280 285

gcc cca gag tcc aac gtc ctg gtc ctg cag tac cct gac ctg tcc 915  
 Ala Pro Glu Ser Asn Val Leu Val Leu Val Gln Tyr Pro Asp Leu Ser  
 290 295 300

aag ctg tac acc ggt aac cct atc acc atc aag tcc gtc tcc gac aag 963  
 Lys Leu Tyr Thr Gly Asn Pro Ile Thr Ile Lys Ser Val Ser Asp Lys  
 305 310 315

aac cct tac tcc cgt atc ctg aac ggt gac aac atc atc ctg cac atg 1011  
 Asn Pro Tyr Ser Arg Ile Leu Asn Gly Asp Asn Ile Ile Leu His Met  
 320 325 330

ctg tac aac tcc cgt aag tac atg atc atc cgt gac acc gac acc atc 1059  
 Leu Tyr Asn Ser Arg Lys Tyr Met Ile Ile Arg Asp Thr Asp Thr Ile  
 335 340 345 350

tac gcc acc cag ggt ggt gag tgt tcc cag aac tgt gtc tac gcc ctg 1107  
 Tyr Ala Thr Gln Gly Gly Glu Cys Ser Gln Asn Cys Val Tyr Ala Leu  
 355 360 365

aag ctg cag tcc aac ctg ggt aac tac ggt atc ggt atc ttc tcc atc 1155  
 Lys Leu Gln Ser Asn Leu Gly Asn Tyr Gly Ile Gly Ile Phe Ser Ile  
 370 375 380

aag aac atc gtc tcc aag aac aag tac tgc tcc cag atc ttc tcc tcc 1203  
 Lys Asn Ile Val Ser Lys Asn Lys Tyr Cys Ser Gln Ile Phe Ser Ser  
 385 390 395

ttc cgt gag aac acc atg ctg ctg gcc gac atc tac aag cct tgg cgt 1251  
Phe Arg Glu Asn Thr Met Leu Leu Ala Asp Ile Tyr Lys Pro Trp Arg  
400 405 410

ttc tcc ttc aag aac gcc tac act cct gtc gcc gtc acc aac tac gag 1299  
Phe Ser Phe Lys Asn Ala Tyr Thr Pro Val Ala Val Thr Asn Tyr Glu  
415 420 425 430

acc aag ctg ctg tcc acc tcc ttc tgg aag ttc atc tcc cgt gac 1347  
Thr Lys Leu Leu Ser Thr Ser Phe Trp Lys Phe Ile Ser Arg Asp  
435 440 445

cca ggt tgg gtc gag taataggaat tc 1374  
Pro Gly Trp Val Glu  
450

<210> 12  
<211> 451  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 12  
Met Arg Leu Lys Ala Lys Val Asn Glu Ser Phe Glu Asn Thr Met Pro  
1 5 10 15  
Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile  
20 25 30  
Asn Glu Tyr Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln  
35 40 45  
Asn Lys Lys Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val  
50 55 60  
Arg Val Gly Asp Asn Val Gln Leu Asn Thr Ile Tyr Thr Asn Asp Phe  
65 70 75 80  
Lys Leu Ser Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn Asn Asn  
85 90 95  
Ile Leu Tyr Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe Trp Ile  
100 105 110  
Lys Ile Ser Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr Ile Ile  
115 120 125  
Asn Ser Ile Glu Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg Asn Gly  
130 135 140  
Asn Ile Glu Trp Ile Leu Gln Asp Val Asn Arg Lys Tyr Lys Ser Leu  
145 150 155 160  
Ile Phe Asp Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr Asn Lys  
165 170 175  
Trp Phe Phe Val Thr Ile Thr Asn Asn Ile Met Gly Tyr Met Lys Leu  
180 185 190  
Tyr Ile Asn Gly Glu Leu Lys Gln Ser Gln Lys Ile Glu Asp Leu Asp  
195 200 205  
Glu Val Lys Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu Asn Ile  
210 215 220  
Asp Glu Asn Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe Ser Lys  
225 230 235 240

Glu Leu Ser Asn Glu Asp Ile Asn Ile Val Tyr Glu Gly Gln Ile Leu  
                  245                 250                 255  
 Arg Asn Val Ile Lys Asp Tyr Trp Gly Asn Pro Leu Lys Phe Asp Thr  
                  260                 265                 270  
 Glu Tyr Tyr Ile Ile Asn Asp Asn Tyr Ile Asp Arg Tyr Ile Ala Pro  
                  275                 280                 285  
 Glu Ser Asn Val Leu Val Leu Val Gln Tyr Pro Asp Leu Ser Lys Leu  
                  290                 295                 300  
 Tyr Thr Gly Asn Pro Ile Thr Ile Lys Ser Val Ser Asp Lys Asn Pro  
                  305                 310                 315                 320  
 Tyr Ser Arg Ile Leu Asn Gly Asp Asn Ile Ile Leu His Met Leu Tyr  
                  325                 330                 335  
 Asn Ser Arg Lys Tyr Met Ile Ile Arg Asp Thr Asp Thr Ile Tyr Ala  
                  340                 345                 350  
 Thr Gln Gly Gly Glu Cys Ser Gln Asn Cys Val Tyr Ala Leu Lys Leu  
                  355                 360                 365  
 Gln Ser Asn Leu Gly Asn Tyr Gly Ile Gly Ile Phe Ser Ile Lys Asn  
                  370                 375                 380  
 Ile Val Ser Lys Asn Lys Tyr Cys Ser Gln Ile Phe Ser Ser Phe Arg  
                  385                 390                 395                 400  
 Glu Asn Thr Met Leu Leu Ala Asp Ile Tyr Lys Pro Trp Arg Phe Ser  
                  405                 410                 415  
 Phe Lys Asn Ala Tyr Thr Pro Val Ala Val Thr Asn Tyr Glu Thr Lys  
                  420                 425                 430  
 Leu Leu Ser Thr Ser Ser Phe Trp Lys Phe Ile Ser Arg Asp Pro Gly  
                  435                 440                 445  
 Trp Val Glu  
                  450

<210> 13  
 <211> 1400  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic construct based on Clostridium botulinum  
 sequence

<221> CDS  
 <222> (10) ... (1356)

<400> 13  
 gaattcacc atg gga gag agt cag caa gaa cta aat tct atg gta act gat 51  
 Met Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr Asp  
       1              5                 10

acc cta aat aat agt att cct ttt aag ctt tct tct tat aca gat gat 99  
 Thr Leu Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp Asp  
   15              20                 25                 30

aaa att tta att tcc tac ttc aac aag ttc ttc aag aga att aag tct 147  
 Lys Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser  
       35              40                 45

tct tcc gtt tta aac atg aga tac aag aat gat aaa tac gtc gac act 195  
 Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr

50	55	60	
tcc ggt tac gac tcc aat atc aac att aac ggt gac gtg tac aag tac Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr 65	70	75	243
cca act aac aaa aac caa ttc ggt atc tac aac gac aag ctt tcc gag Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Ser Glu 80	85	90	291
gtc aac atc tct caa aac gac tac att atc tac gac aac aag tac aag Val Asn Ile Ser Gln Asn Asp Tyr Ile Tyr Asp Asn Lys Tyr Lys 95	100	105	339
aac ttc tct att tct ttc tgg gtc agg att cct aac tac gac aac aag Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys 115	120	125	387
atc gtc aac gtt aac aac gag tac act atc atc aac tgt atg aga gac Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp 130	135	140	435
aac aac tcc ggt tgg aag gtc tct ctt aac cac aac gag atc att tgg Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp 145	150	155	483
acc ttg caa gac aac gca ggt att aac caa aag tta gca ttc aac tac Thr Leu Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr 160	165	170	531
ggc aac gca aac ggt att tct gac tac atc aac aag tgg att ttc gtc Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val 175	180	185	579
act atc act aac gac aga tta ggt gac tct aag ctt tac att aac ggt Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly 195	200	205	627
aac tta atc gac caa aag tcc att tta aac tta ggt aac att cac gtt Asn Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val 210	215	220	675
tct gac aac atc tta ttc aag atc gtt aac tgc agt tac acc aga tac Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr 225	230	235	723
att ggc att aga tac ttc aac att ttc gac aag gag tta gac gag acc Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr 240	245	250	771
gag att caa act tta tac agc aac gaa cct aac acc aat att ttg aag Glu Ile Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu Lys 255	260	265	819
gac ttc tgg ggt aac tac ttg ctt tac gac aag gaa tac tac tta tta Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu 275	280	285	867

aac gtg tta aag cca aac aac ttc att gat agg aga aag gat tct act		915
Asn Val Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser Thr		
290	295	300
tta agc att aac aac atc aga agc act att ctt tta gct aac aga tta		963
Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu		
305	310	315
tac tct ggt atc aag gtt aag atc caa aga gtt aac aac tct tct act		1011
Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser Thr		
320	325	330
aac gat aac ctt gtt aga aag aac gat cag gtc tat att aac ttc gtc		1059
Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe Val		
335	340	345
350		
gct agc aag act cac tta ttc cca tta tat gct gat acc gct acc acc		1107
Ala Ser Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr Thr		
355	360	365
aac aag gag aag acc atc aag atc tcc tcc tct ggc aac aga ttt aac		1155
Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe Asn		
370	375	380
caa gtc gtc gtt atg aac tcc gtc ggt aac aac tgt acc atg aac ttt		1203
Gln Val Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn Phe		
385	390	395
aaa aat aat aat gga aat aat att ggg ttg tta ggt ttc aag gca gat		1251
Lys Asn Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp		
400	405	410
act gta gtt gct agt act tgg tat tat acc cac atg aga gat cac acc		1299
Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His Thr		
415	420	425
430		
aac agc aat gga tgt ttt tgg aac ttt att tct gaa gaa cat gga tgg		1347
Asn Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp		
435	440	445
caa gaa aaa taataggat ccgcggccgc acgcgtcccg ggactagtga		1396
Gln Glu Lys		
 atcc		1400
<210> 14		
<211> 449		
<212> PRT		
<213> Artificial Sequence		
 <220>		
<223> Synthetic Construct		
 <400> 14		
Met Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr Asp Thr Leu		

1	5	10	15
Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp Asp Lys Ile			
20	25	30	
Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser Ser Ser			
35	40	45	
Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr Ser Gly			
50	55	60	
Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr Pro Thr			
65	70	75	80
Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Ser Glu Val Asn			
85	90	95	
Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys Asn Phe			
100	105	110	
Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys Ile Val			
115	120	125	
Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp Asn Asn			
130	135	140	
Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp Thr Leu			
145	150	155	160
Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr Gly Asn			
165	170	175	
Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val Thr Ile			
180	185	190	
Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly Asn Leu			
195	200	205	
Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val Ser Asp			
210	215	220	
Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr Ile Gly			
225	230	235	240
Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr Glu Ile			
245	250	255	
Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu Lys Asp Phe			
260	265	270	
Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu Asn Val			
275	280	285	
Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser Thr Leu Ser			
290	295	300	
Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu Tyr Ser			
305	310	315	320
Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser Thr Asn Asp			
325	330	335	
Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe Val Ala Ser			
340	345	350	
Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr Thr Asn Lys			
355	360	365	
Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe Asn Gln Val			
370	375	380	
Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn Phe Lys Asn			
385	390	395	400
Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp Thr Val			
405	410	415	
Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His Thr Asn Ser			
420	425	430	
Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp Gln Glu			
435	440	445	
Lys			

<210> 15  
<211> 1317  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<221> CDS  
<222> (10)...(1305)

<400> 15

gaattcacg atg tcc tac acc aac gac aag atc ctg atc ttg tac ttc aac 51  
Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn  
1 5 10

aag ctg tac aag aag atc aag gac aac tcc atc ttg gac atg aga tac 99  
Lys Leu Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr  
15 20 25 30

gaa aac aat aag ttc atc gac atc tcc ggt tac ggt tcc aac atc tcc 147  
Glu Asn Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser  
35 40 45

atc aac ggt gac gtc tac atc tac tcc acc aat aga aac cag ttc gga 195  
Ile Asn Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly  
50 55 60

atc tac tcc tcc aag cct tcc gag gtc aac atc gct cag aac aac gac 243  
Ile Tyr Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp  
65 70 75

atc atc tac aac gga aga tac cag aac ttc tcc atc tcc ttc tgg gtc 291  
Ile Ile Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val  
80 85 90

cgt atc cca aag tac ttc aac aag gtc aac ctg aat aac gag tac acc 339  
Arg Ile Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr  
95 100 105 110

atc atc gac tgc atc cgt aac aat aac tcc gga tgg aag atc tcc ctg 387  
Ile Ile Asp Cys Ile Arg Asn Asn Ser Gly Trp Lys Ile Ser Leu  
115 120 125

aac tac aac aag atc atc tgg acc ctg cag gac acc gcc ggt aac aat 435  
Asn Tyr Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn  
130 135 140

cag aag ttg gtc ttc aac tac acc cag atg atc tcc atc tcc gac tac 483  
Gln Lys Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr  
145 150 155

atc aac aag tgg atc ttc gtc acc atc acc aat aac cgt ttg gga aac 531  
Ile Asn Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn  
160 165 170

tcc aga atc tac atc aac ggt aac ttg atc gac gag aag tcc atc tcc		579
Ser Arg Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser		
175	180	185
190		
aac ttg ggt gac atc cac gtc tcc gac aac att ttg ttc aag atc gtc		627
Asn Leu Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val		
195	200	205
ggt tgt aac gac acc cgt tac gtc ggg atc cgt tac ttc aaa gtc ttc		675
Gly Cys Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe		
210	215	220
gac act gag ttg ggt aag acc gag atc gag acc ttg tac tcc gac gag		723
Asp Thr Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu		
225	230	235
cct gac cca tcc atc ctg aag gac ttc tgg ggt aac tac ctg ctg tac		771
Pro Asp Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr		
240	245	250
aac aaa cgt tac tac ttg ctg aac ttg ttg cgt acc gac aag tcc atc		819
Asn Lys Arg Tyr Tyr Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile		
255	260	265
270		
acc cag aac tcc aac ttc ttg aac atc aac cag cag aga ggt gtc tac		867
Thr Gln Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr		
275	280	285
cag aag cca aac atc ttc tcc aac acc aga ttg tac acc gga gtc gag		915
Gln Lys Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu		
290	295	300
gtc att atc aga aag aac gga tct act gat att tcc aac acc gat aac		963
Val Ile Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn		
305	310	315
ttc gtc aga aag aac gat ctg gct tac atc aac gtt gtc gac aga gat		1011
Phe Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp		
320	325	330
gtc gaa tac cgt ctg tac gcc gat atc tct atc gcc aaa cct gaa aag		1059
Val Glu Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys		
335	340	345
350		
atc atc aag ctg atc cgt acc tct aac tct aac tct ctg gga caa		1107
Ile Ile Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln		
355	360	365
atc atc gtc atg gac tcc atc ggt aat aac tgt acc atg aac ttc cag		1155
Ile Ile Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln		
370	375	380
aac aac aac ggt gga aac atc ggt ttg ttg ggt ttc cac tcc aac aac		1203
Asn Asn Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn		
385	390	395

ttg gtc gct tcc tcc tgg tac tac aac aac atc cgt aag aac acc tcc	1251		
Leu Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser			
400	405	410	
tcc aac ggt tgc ttc tgg tcc ttc atc tcc aag gag cac ggt tgg cag	1299		
Ser Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln			
415	420	425	430
gag aac taataggaat tc	1317		
Glu Asn			

<210> 16  
<211> 432  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 16			
Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu			
1	5	10	15
Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn			
20	25	30	
Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn			
35	40	45	
Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr			
50	55	60	
Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile			
65	70	75	80
Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile			
85	90	95	
Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile			
100	105	110	
Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr			
115	120	125	
Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys			
130	135	140	
Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn			
145	150	155	160
Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg			
165	170	175	
Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu			
180	185	190	
Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys			
195	200	205	
Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr			
210	215	220	
Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp			
225	230	235	240
Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys			
245	250	255	
Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln			
260	265	270	
Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys			

275	280	285
Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile		
290	295	300
Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val		
305	310	315
Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu		
325	330	335
Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile		
340	345	350
Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile		
355	360	365
Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn		
370	375	380
Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val		
385	390	395
Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn		
405	410	415
Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn		
420	425	430

<210> 17  
<211> 1368  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<221> CDS  
<222> (10)...(1356)

<400> 17  
gaattcacg atg aag gac acc atc ctg atc cag gtc ttc aac aac tac atc 51  
Met Lys Asp Thr Ile Leu Ile Gln Val Phe Asn Asn Tyr Ile  
1 5 10

tcc aac atc tcc tcc aac gcc atc ctg tcc ctg tcc tac cgt ggt ggt 99  
Ser Asn Ile Ser Ser Asn Ala Ile Leu Ser Leu Ser Tyr Arg Gly Gly  
15 20 25 30

cgt ctg atc gac tcc tcc ggt tac gga gcc acc atg aac gtc ggt tcc 147  
Arg Leu Ile Asp Ser Ser Gly Tyr Gly Ala Thr Met Asn Val Gly Ser  
35 40 45

gac gtc atc ttc aac gac atc ggt aac ggt cag ttc aag ctg aac aac 195  
Asp Val Ile Phe Asn Asp Ile Gly Asn Gly Gln Phe Lys Leu Asn Asn  
50 55 60

tcc gag aac tcc aac atc acc gcc cac cag tcc aag ttc gtc gtc tac 243  
Ser Glu Asn Ser Asn Ile Thr Ala His Gln Ser Lys Phe Val Val Tyr  
65 70 75

gac tcc atg ttc gac aac ttc tcc atc aac ttc tgg gtc cgt acc cca 291  
Asp Ser Met Phe Asp Asn Phe Ser Ile Asn Phe Trp Val Arg Thr Pro  
80 85 90

aag tac aac aac aac gac atc cag acc tac ctg cag aac gag tac acc		339
Lys Tyr Asn Asn Asn Asp Ile Gln Thr Tyr Leu Gln Asn Glu Tyr Thr		
95	100	105
110		
atc atc tcc tgt atc aag aac gac tcc ggt tgg aag gtc tcc atc aag		387
Ile Ile Ser Cys Ile Lys Asn Asp Ser Gly Trp Lys Val Ser Ile Lys		
115	120	125
gga aac cgt atc atc tgg acc ctg atc gac gtc aac gcc aag tcc aag		435
Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Val Asn Ala Lys Ser Lys		
130	135	140
tcc atc ttc ttc gag tac tcc atc aag gac aac atc tcc gac tac atc		483
Ser Ile Phe Phe Glu Tyr Ser Ile Lys Asp Asn Ile Ser Asp Tyr Ile		
145	150	155
aac aag tgg ttc tcc atc acc atc acc aac gac cgt ctg ggt aac gcc		531
Asn Lys Trp Phe Ser Ile Thr Ile Thr Asn Asp Arg Leu Gly Asn Ala		
160	165	170
aac atc tac atc aac ggt tcc ctg aag aag tcc gag aag atc ctg aac		579
Asn Ile Tyr Ile Asn Gly Ser Leu Lys Ser Glu Lys Ile Leu Asn		
175	180	185
190		
ctg gac cgt atc aac tcc tcc aac gac atc gac ttc aag ctg atc aac		627
Leu Asp Arg Ile Asn Ser Asn Asp Ile Asp Phe Lys Leu Ile Asn		
195	200	205
tgt acc gac acc acc aag ttc gtc tgg atc aag gac ttc aac atc ttc		675
Cys Thr Asp Thr Thr Lys Phe Val Trp Ile Lys Asp Phe Asn Ile Phe		
210	215	220
ggt cgt gag ctg aac gcc acc gag gtc tcc tcc ctg tac tgg atc cag		723
Gly Arg Glu Leu Asn Ala Thr Glu Val Ser Ser Leu Tyr Trp Ile Gln		
225	230	235
tcc tcc acc aac acc ctg aag gac ttc tgg gga aac cca ctg cgt tac		771
Ser Ser Thr Asn Thr Leu Lys Asp Phe Trp Gly Asn Pro Leu Arg Tyr		
240	245	250
gac acc cag tac tac ctg ttc aac cag ggt atg cag aac atc tac atc		819
Asp Thr Gln Tyr Tyr Leu Phe Asn Gln Gly Met Gln Asn Ile Tyr Ile		
255	260	265
270		
aag tac ttc tcc aag gcc tcc atg ggt gag acc gcc cct cgt acc aac		867
Lys Tyr Phe Ser Lys Ala Ser Met Gly Glu Thr Ala Pro Arg Thr Asn		
275	280	285
ttc aac aac gcc gcc atc aac tac cag aac ctg tac ctg ggt ctg cgt		915
Phe Asn Asn Ala Ala Ile Asn Tyr Gln Asn Leu Tyr Leu Gly Leu Arg		
290	295	300
ttc atc atc aag aag gcc tcc aac tcc cgt aac atc aac aac gac aac		963
Phe Ile Ile Lys Lys Ala Ser Asn Ser Arg Asn Ile Asn Asn Asp Asn		
305	310	315
atc gtc cgt gag ggt gac tac atc tac ctg aac atc gac aac atc tcc		1011

Ile Val Arg Glu Gly Asp Tyr Ile Tyr Leu Asn Ile Asp Asn Ile Ser				
320	325	330		
gac gag tcc tac cgt gtc tac gtc ctg gtc aac tcc aag gag atc cag				1059
Asp Glu Ser Tyr Arg Val Tyr Val Leu Val Asn Ser Lys Glu Ile Gln				
335	340	345	350	
acc cag ctg ttc ctg gcc cca atc aac gac gac cct acc ttc tac gac				1107
Thr Gln Leu Phe Leu Ala Pro Ile Asn Asp Asp Pro Thr Phe Tyr Asp				
355	360	365		
gtc ctg cag atc aag aag tac tac gag aag acc acc tac aac tgt cag				1155
Val Leu Gln Ile Lys Lys Tyr Tyr Glu Lys Thr Thr Tyr Asn Cys Gln				
370	375	380		
atc ctg tgc gag aag gac acc aag acc ttc gga ctg ttc ggt atc ggt				1203
Ile Leu Cys Glu Lys Asp Thr Lys Thr Phe Gly Leu Phe Gly Ile Gly				
385	390	395		
aag ttc gtc aag gac tac ggt tac gtc tgg gac acc tac gac aac tac				1251
Lys Phe Val Lys Asp Tyr Gly Tyr Val Trp Asp Thr Tyr Asp Asn Tyr				
400	405	410		
ttc tgt atc tcc cag tgg tac ctg cgt atc tcc gag aac atc aac				1299
Phe Cys Ile Ser Gln Trp Tyr Leu Arg Arg Ile Ser Glu Asn Ile Asn				
415	420	425	430	
aag ctg cgt ctg gga tgt aac tgg cag ttc atc cca gtc gac gag ggt				1347
Lys Leu Arg Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Glu Gly				
435	440	445		
tgg acc gag taataggaat tc				1368
Trp Thr Glu				

<210> 18  
<211> 449  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 18				
Met Lys Asp Thr Ile Leu Ile Gln Val Phe Asn Asn Tyr Ile Ser Asn				
1	5	10	15	
Ile Ser Ser Asn Ala Ile Leu Ser Leu Ser Tyr Arg Gly Gly Arg Leu				
20	25	30		
Ile Asp Ser Ser Gly Tyr Gly Ala Thr Met Asn Val Gly Ser Asp Val				
35	40	45		
Ile Phe Asn Asp Ile Gly Asn Gly Gln Phe Lys Leu Asn Asn Ser Glu				
50	55	60		
Asn Ser Asn Ile Thr Ala His Gln Ser Lys Phe Val Val Tyr Asp Ser				
65	70	75	80	
Met Phe Asp Asn Phe Ser Ile Asn Phe Trp Val Arg Thr Pro Lys Tyr				
85	90	95		

Asn Asn Asn Asp Ile Gln Thr Tyr Leu Gln Asn Glu Tyr Thr Ile Ile  
           100                 105                 110  
 Ser Cys Ile Lys Asn Asp Ser Gly Trp Lys Val Ser Ile Lys Gly Asn  
           115                 120                 125  
 Arg Ile Ile Trp Thr Leu Ile Asp Val Asn Ala Lys Ser Lys Ser Ile  
           130                 135                 140  
 Phe Phe Glu Tyr Ser Ile Lys Asp Asn Ile Ser Asp Tyr Ile Asn Lys  
           145                 150                 155                 160  
 Trp Phe Ser Ile Thr Ile Thr Asn Asp Arg Leu Gly Asn Ala Asn Ile  
           165                 170                 175  
 Tyr Ile Asn Gly Ser Leu Lys Lys Ser Glu Lys Ile Leu Asn Leu Asp  
           180                 185                 190  
 Arg Ile Asn Ser Ser Asn Asp Ile Asp Phe Lys Leu Ile Asn Cys Thr  
           195                 200                 205  
 Asp Thr Thr Lys Phe Val Trp Ile Lys Asp Phe Asn Ile Phe Gly Arg  
           210                 215                 220  
 Glu Leu Asn Ala Thr Glu Val Ser Ser Leu Tyr Trp Ile Gln Ser Ser  
           225                 230                 235                 240  
 Thr Asn Thr Leu Lys Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr  
           245                 250                 255  
 Gln Tyr Tyr Leu Phe Asn Gln Gly Met Gln Asn Ile Tyr Ile Lys Tyr  
           260                 265                 270  
 Phe Ser Lys Ala Ser Met Gly Glu Thr Ala Pro Arg Thr Asn Phe Asn  
           275                 280                 285  
 Asn Ala Ala Ile Asn Tyr Gln Asn Leu Tyr Leu Gly Leu Arg Phe Ile  
           290                 295                 300  
 Ile Lys Lys Ala Ser Asn Ser Arg Asn Ile Asn Asn Asp Asn Ile Val  
           305                 310                 315                 320  
 Arg Glu Gly Asp Tyr Ile Tyr Leu Asn Ile Asp Asn Ile Ser Asp Glu  
           325                 330                 335  
 Ser Tyr Arg Val Tyr Val Leu Val Asn Ser Lys Glu Ile Gln Thr Gln  
           340                 345                 350  
 Leu Phe Leu Ala Pro Ile Asn Asp Asp Pro Thr Phe Tyr Asp Val Leu  
           355                 360                 365  
 Gln Ile Lys Lys Tyr Tyr Glu Lys Thr Thr Tyr Asn Cys Gln Ile Leu  
           370                 375                 380  
 Cys Glu Lys Asp Thr Lys Thr Phe Gly Leu Phe Gly Ile Gly Lys Phe  
           385                 390                 395                 400  
 Val Lys Asp Tyr Gly Tyr Val Trp Asp Thr Tyr Asp Asn Tyr Phe Cys  
           405                 410                 415  
 Ile Ser Gln Trp Tyr Leu Arg Arg Ile Ser Glu Asn Ile Asn Lys Leu  
           420                 425                 430  
 Arg Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Glu Gly Trp Thr  
           435                 440                 445  
 Glu

<210> 19  
 <211> 1242  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<221> CDS

<222> (1) . . . (1239)

<400> 19  
atg gct ctg aac gac ctg tgc atc aaa gtt aac aac tgg gac ctg ttc 48  
Met Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe  
1 5 10 15

ttc tcc ccg tct gaa gac aac ttc act aac gac ctg aac aaa ggc gaa 96  
Phe Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu  
20 25 30

gaa atc acc tcc gac act aac atc gaa gct gct gaa gaa aac atc tct 144  
Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser  
35 40 45

ctg gac ctg atc cag cag tac tac ctg act ttc aac ttc gac aac gaa 192  
Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu  
50 55 60

ccg gaa aac atc tcc atc gaa aac ctg tct tcc gac atc atc ggt cag 240  
Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln  
65 70 75 80

ctg gaa ctg atg ccg aac atc gaa cgc ttc ccg aac ggc aag aaa tac 288  
Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr  
85 90 95

gaa ctg gac aaa tac acc atg ttc cac tac ctg cgt gct cag gaa ttc 336  
Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe  
100 105 110

gaa cac ggt aaa tct cgt atc gct ctg act aac tcc gtt aac gaa gct 384  
Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala  
115 120 125

ctg ctg aac ccg tct cgc gtt tac acc ttc ttc tct tcc gac tac gtt 432  
Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val  
130 135 140

aag aaa gtt aac aaa gct act gaa gct gct atg ttc ctg ggt tgg gtt 480  
Lys Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val  
145 150 155 160

gaa cag ctg gtt tac gac ttc acc gac gaa act tct gaa gtt tcc acc 528  
Glu Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr  
165 170 175

act gac aaa atc gct gac atc act atc atc atc ccg tac atc ggc ccg 576  
Thr Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro  
180 185 190

gct ctg aac atc ggt aac atg ctg tac aaa gac gac ttc gtt ggt gct 624  
Ala Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala  
195 200 205

ctg atc ttc tct ggc gct gtt atc ctg ctg gaa ttc atc ccg gaa atc 672  
Leu Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile

210	215	220	
gct atc ccg gtt ctg ggt acc ttc gct ctg gtt tcc tac atc gct aac Ala Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn 225 230 235 240			720
aaa gtt ctg act gtt cag acc atc gac aac gct ctg tct aaa cgt aac Lys Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn 245 250 255			768
gaa aaa tgg gac gaa gtt tac aaa tac atc gtt act aac tgg ctg gct Glu Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala 260 265 270			816
aaa gtt aac act cag atc gac ctg atc cgt aag aag atg aaa gaa gct Lys Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala 275 280 285			864
ctg gaa aac cag gct gaa gct act aaa gct atc atc aac tac cag tac Leu Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr 290 295 300			912
aac cag tac acc gaa gaa aag aac aac atc aac ttc aac atc gat Asn Gln Tyr Thr Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp 305 310 315 320			960
gac ctg tcc tct aaa ctg aac gaa tcc atc aac aaa gct atg atc aac Asp Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn 325 330 335			1008
atc aac aaa ttc ctg aac cag tgc tct gtt tcc tac ctg atg aac tct Ile Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser 340 345 350			1056
atg atc ccg tac ggc gtt aaa cgc ctg gaa gac ttc gac gct tcc ctg Met Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu 355 360 365			1104
aaa gac gct ctg ctg aaa tac atc cgt gac aac tac ggt act ctg atc Lys Asp Ala Leu Leu Lys Tyr Ile Arg Asp Asn Tyr Gly Thr Leu Ile 370 375 380			1152
ggc cag gtt gac cgt ctg aaa gac aag gtt aac aac acc ctg tct act Gly Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr 385 390 395 400			1200
gac atc ccg ttc cag ctg tcc aaa tac gtt gac aac cag taa Asp Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln 405 410			1242

<210> 20  
<211> 413  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 20

Met Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe  
1 5 10 15  
Phe Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu  
20 25 30  
Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser  
35 40 45  
Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu  
50 55 60  
Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln  
65 70 75 80  
Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr  
85 90 95  
Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe  
100 105 110  
Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala  
115 120 125  
Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val  
130 135 140  
Lys Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val  
145 150 155 160  
Glu Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr  
165 170 175  
Thr Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro  
180 185 190  
Ala Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala  
195 200 205  
Leu Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile  
210 215 220  
Ala Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn  
225 230 235 240  
Lys Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn  
245 250 255  
Glu Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala  
260 265 270  
Lys Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala  
275 280 285  
Leu Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr  
290 295 300  
Asn Gln Tyr Thr Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp  
305 310 315 320  
Asp Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn  
325 330 335  
Ile Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser  
340 345 350  
Met Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu  
355 360 365  
Lys Asp Ala Leu Leu Lys Tyr Ile Arg Asp Asn Tyr Gly Thr Leu Ile  
370 375 380  
Gly Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr  
385 390 395 400  
Asp Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln  
405 410

<210> 21  
 <211> 1242  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<221> CDS  
 <222> (1) ... (1239)

<400> 21

atg	gct	cca	gga	atc	tgt	atc	gac	gtc	gac	aac	gag	gac	ttg	ttc	ttc	48
Met	Ala	Pro	Gly	Ile	Cys	Ile	Asp	Val	Asp	Asn	Glu	Asp	Leu	Phe	Phe	
1	5					10							15			

atc gct gac aag aac tcc ttc tcc gac gac ttg tcc aag aac gag aga 96  
 Ile Ala Asp Lys Asn Ser Phe Ser Asp Asp Leu Ser Lys Asn Glu Arg  
 20 25 30

atc gag tac aac acc cag tcc aac tac atc gag aac gac ttc cca atc 144  
 Ile Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile  
 35 40 45

aac gag ttg atc ttg gac acc gac ttg atc tcc aag atc gag ttg cca 192  
 Asn Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro  
 50 55 60

tcc gag aac acc gag tcc ttg act gac ttc aac gtc gac gtc cca gtc 240  
 Ser Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val  
 65 70 75 80

tac gag aag caa cca gct atc aag aag att ttc acc gac gag aac acc 288  
 Tyr Glu Lys Gln Pro Ala Ile Lys Ile Phe Thr Asp Glu Asn Thr  
 85 90 95

atc ttc caa tac ctg tac tct cag acc ttc cct ttg gac atc aga gac 336  
 Ile Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp  
 100 105 110

atc tcc ttg acc tct tcc ttc gac gac gcc ctg ttc tcc aac aag 384  
 Ile Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys  
 115 120 125

gtc tac tcc ttc tcc atg gac tac atc aag act gct aac aag gtc 432  
 Val Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val  
 130 135 140

gtc gag gcc ggt ttg ttc gct ggt tgg gtc aag cag atc gtc aac gat 480  
 Val Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp  
 145 150 155 160

ttc gtc atc gag gct aac aag tcc aac acc atg gac aag att gcc gac 528  
 Phe Val Ile Glu Ala Asn Lys Ser Asn Thr Met Asp Lys Ile Ala Asp  
 165 170 175

atc tcc ttg att gtc cca tac atc ggt ttg gcc ttg aac gtc ggt aac 576

Ile Ser Leu Ile Val Pro Tyr Ile Gly Leu Ala Leu Asn Val Gly Asn			
180	185	190	
gag acc gcc aag ggt aac ttc gag aac gct ttc gag atc gct ggt gcc 624			
Glu Thr Ala Lys Gly Asn Phe Glu Asn Ala Phe Glu Ile Ala Gly Ala			
195	200	205	
tcc atc ttg ttg gag ttc atc cca gag ttg ttg atc cca gtc gtc ggt 672			
Ser Ile Leu Leu Glu Phe Ile Pro Glu Leu Leu Ile Pro Val Val Gly			
210	215	220	
gcc ttc ttg ttg gag tcc tac atc gac aac aag aac aag atc atc aag 720			
Ala Phe Leu Leu Glu Ser Tyr Ile Asp Asn Lys Asn Lys Ile Ile Lys			
225	230	235	240
acc atc gac aac gct ttg acc aag aga aac gag aag tgg tcc gac atg 768			
Thr Ile Asp Asn Ala Leu Thr Lys Arg Asn Glu Lys Trp Ser Asp Met			
245	250	255	
tac ggt ttg atc gtc gcc caa tgg ttg tcc acc gtc aac acc caa ttc 816			
Tyr Gly Leu Ile Val Ala Gln Trp Leu Ser Thr Val Asn Thr Gln Phe			
260	265	270	
tac acc atc aag gag ggt atg tac aag gcc ttg aac tac cag gcc caa 864			
Tyr Thr Ile Lys Glu Gly Met Tyr Lys Ala Leu Asn Tyr Gln Ala Gln			
275	280	285	
gct ttg gag gag atc atc aag tac aga tac aac atc tac tcc gag aag 912			
Ala Leu Glu Glu Ile Ile Lys Tyr Arg Tyr Asn Ile Tyr Ser Glu Lys			
290	295	300	
gag aag tcc aac att aac atc gac ttc aac gac atc aac tcc aag ctg 960			
Glu Lys Ser Asn Ile Asn Ile Asp Phe Asn Asp Ile Asn Ser Lys Leu			
305	310	315	320
aac gag ggt att aac cag gcc atc gac aac atc aac aac ttc atc aac 1008			
Asn Glu Gly Ile Asn Gln Ala Ile Asp Asn Ile Asn Asn Phe Ile Asn			
325	330	335	
ggt tgt tcc gtc tcc tac ttg atg aag aag atg att cca ttg gcc gtc 1056			
Gly Cys Ser Val Ser Tyr Leu Met Lys Lys Met Ile Pro Leu Ala Val			
340	345	350	
gag aag ttg ttg gac ttc gac aac acc ctg aag aag aac ttg ttg aac 1104			
Glu Lys Leu Leu Asp Phe Asp Asn Thr Leu Lys Lys Asn Leu Leu Asn			
355	360	365	
tac atc gac gag aac aag ttg tac ttg atc ggt tcc gct gag tac gag 1152			
Tyr Ile Asp Glu Asn Lys Leu Tyr Leu Ile Gly Ser Ala Glu Tyr Glu			
370	375	380	
aag tcc aag gtc aac aag tac ttg aag acc atc atg cca ttc gac ttg 1200			
Lys Ser Lys Val Asn Lys Tyr Leu Lys Thr Ile Met Pro Phe Asp Leu			
385	390	395	400
tcc atc tac acc aac gac acc atc ttg atc gag atg ttc taa 1242			
Ser Ile Tyr Thr Asn Asp Thr Ile Leu Ile Glu Met Phe			

<210> 22  
<211> 413  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 22  
Met Ala Pro Gly Ile Cys Ile Asp Val Asp Asn Glu Asp Leu Phe Phe  
1               5               10               15  
Ile Ala Asp Lys Asn Ser Phe Ser Asp Asp Leu Ser Lys Asn Glu Arg  
20               25               30  
Ile Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile  
35               40               45  
Asn Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro  
50               55               60  
Ser Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val  
65               70               75               80  
Tyr Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr  
85               90               95  
Ile Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp  
100              105              110  
Ile Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys  
115              120              125  
Val Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val  
130              135              140  
Val Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp  
145              150              155              160  
Phe Val Ile Glu Ala Asn Lys Ser Asn Thr Met Asp Lys Ile Ala Asp  
165              170              175  
Ile Ser Leu Ile Val Pro Tyr Ile Gly Leu Ala Leu Asn Val Gly Asn  
180              185              190  
Glu Thr Ala Lys Gly Asn Phe Glu Asn Ala Phe Glu Ile Ala Gly Ala  
195              200              205  
Ser Ile Leu Leu Glu Phe Ile Pro Glu Leu Leu Ile Pro Val Val Gly  
210              215              220  
Ala Phe Leu Leu Glu Ser Tyr Ile Asp Asn Lys Asn Lys Ile Ile Lys  
225              230              235              240  
Thr Ile Asp Asn Ala Leu Thr Lys Arg Asn Glu Lys Trp Ser Asp Met  
245              250              255  
Tyr Gly Leu Ile Val Ala Gln Trp Leu Ser Thr Val Asn Thr Gln Phe  
260              265              270  
Tyr Thr Ile Lys Glu Gly Met Tyr Lys Ala Leu Asn Tyr Gln Ala Gln  
275              280              285  
Ala Leu Glu Glu Ile Ile Lys Tyr Arg Tyr Asn Ile Tyr Ser Glu Lys  
290              295              300  
Glu Lys Ser Asn Ile Asn Ile Asp Phe Asn Asp Ile Asn Ser Lys Leu  
305              310              315              320  
Asn Glu Gly Ile Asn Gln Ala Ile Asp Asn Ile Asn Asn Phe Ile Asn  
325              330              335  
Gly Cys Ser Val Ser Tyr Leu Met Lys Lys Met Ile Pro Leu Ala Val  
340              345              350  
Glu Lys Leu Leu Asp Phe Asp Asn Thr Leu Lys Lys Asn Leu Leu Asn

355	360	365
Tyr Ile Asp Glu Asn Lys Leu Tyr Leu Ile Gly Ser Ala Glu Tyr Glu		
370	375	380
Lys Ser Lys Val Asn Lys Tyr Leu Lys Thr Ile Met Pro Phe Asp Leu		
385	390	395
Ser Ile Tyr Thr Asn Asp Thr Ile Leu Ile Glu Met Phe		
405	410	

<210> 23  
<211> 1200  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<221> CDS  
<222> (1) ... (1197)

<400> 23						
atg tcc ctg tac aac aag acc ctt gac tgt aga gag ctg ctg gtg aag						48
Met Ser Leu Tyr Asn Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys						
1	5	10	15			

aac act gac ctg cca ttc atc ggt gac atc agt gac gtg aag act gac						96
Asn Thr Asp Leu Pro Phe Ile Gly Asp Ile Ser Asp Val Lys Thr Asp						
20	25	30				

atc ttc ctg cgt aag gac atc aac gag gag act gag gtg atc tac tac						144
Ile Phe Leu Arg Lys Asp Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr						
35	40	45				

cca gac aac gtg tca gta gac caa gtg atc ctc agt aag aac acc tcc						192
Pro Asp Asn Val Ser Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser						
50	55	60				

gag cat gga caa cta gac ctg ctc tac cct agt atc gac agt gag agt						240
Glu His Gly Gln Leu Asp Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser						
65	70	75	80			

gag atc ctg cca ggg gag aat caa gtc ttc tac gac aac cgt acc cag						288
Glu Ile Leu Pro Gly Glu Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln						
85	90	95				

aac gtg gac tac ctg aac tcc tac tac tac cta gag tct cag aag ctg						336
Asn Val Asp Tyr Leu Asn Ser Tyr Tyr Leu Glu Ser Gln Lys Leu						
100	105	110				

agt gac aac gtg gag gac ttc act ttc acg cgt tca atc gag gag gct						384
Ser Asp Asn Val Glu Asp Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala						
115	120	125				

ctg gac aac agt gca aag gtg tac act tac ttc cct acc ctg gct aac						432
Leu Asp Asn Ser Ala Lys Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn						
130	135	140				

aag gtg aat gcc ggt gtg caa ggt ggt ctg ttc ctg atg tgg gca aac Lys Val Asn Ala Gly Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn 145 150 155 160	480
gac gtg gtt gag gac ttc act acc aac atc ctg cgt aag gac aca ctg Asp Val Val Glu Asp Phe Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu 165 170 175	528
gac aag atc tca gat gtg tca gct atc atc ccc tac atc gga ccc gca Asp Lys Ile Ser Asp Val Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala 180 185 190	576
ctg aac atc tcc aac tct gtg cgt cgt gga aac ttc act gag gca ttc Leu Asn Ile Ser Asn Ser Val Arg Arg Gly Asn Phe Thr Glu Ala Phe 195 200 205	624
gca gtc act ggt gtc acc atc ctg ctg gag gca ttc cct gag ttc aca Ala Val Thr Gly Val Thr Ile Leu Leu Glu Ala Phe Pro Glu Phe Thr 210 215 220	672
atc cct gct ctg ggt gca ttc gtg atc tac agt aag gtc cag gag cga Ile Pro Ala Leu Gly Ala Phe Val Ile Tyr Ser Lys Val Gln Glu Arg 225 230 235 240	720
aac gag atc atc aag acc atc gac aac tgt ctg gag cag agg atc aag Asn Glu Ile Ile Lys Thr Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys 245 250 255	768
aga tgg aag gac tcc tac gag tgg atg atg gga acg tgg ttg tcc agg Arg Trp Lys Asp Ser Tyr Glu Trp Met Met Gly Thr Trp Leu Ser Arg 260 265 270	816
atc atc acc cag ttc aac aac atc tcc tac cag atg tac gac tcc ctg Ile Ile Thr Gln Phe Asn Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu 275 280 285	864
aac tac cag gca ggt gca atc aag gct aag atc gac ctg gag tac aag Asn Tyr Gln Ala Gly Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys 290 295 300	912
aag tac tcc gga agc gac aag gag aac atc aag agc cag gtt gag aac Lys Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn 305 310 315 320	960
ctg aag aac agt ctg gac gtc aag atc tcg gag gca atg aac aac atc Leu Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile 325 330 335	1008
aac aag ttc atc cga gag tgc tcc gtc acc tac ctg ttc aag aac atg Asn Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met 340 345 350	1056
ctg cct aag gtc atc gac gag ctg aac gag ttc gac cga aac acc aag Leu Pro Lys Val Ile Asp Glu Leu Asn Glu Phe Asp Arg Asn Thr Lys 355 360 365	1104
gca aag ctg atc aac ctg atc gac tcc cat aac atc atc ctg gtc ggt	1152

Ala Lys Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly  
370 375 380

gag gtc gac aag ctg aag gca aag gta aac aac agc ttc cag aac 1197  
Glu Val Asp Lys Leu Lys Ala Lys Val Asn Asn Ser Phe Gln Asn  
385 390 395

taa 1200

<210> 24  
<211> 399  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 24  
Met Ser Leu Tyr Asn Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys  
1 5 10 15  
Asn Thr Asp Leu Pro Phe Ile Gly Asp Ile Ser Asp Val Lys Thr Asp  
20 25 30  
Ile Phe Leu Arg Lys Asp Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr  
35 40 45  
Pro Asp Asn Val Ser Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser  
50 55 60  
Glu His Gly Gln Leu Asp Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser  
65 70 75 80  
Glu Ile Leu Pro Gly Glu Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln  
85 90 95  
Asn Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu  
100 105 110  
Ser Asp Asn Val Glu Asp Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala  
115 120 125  
Leu Asp Asn Ser Ala Lys Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn  
130 135 140  
Lys Val Asn Ala Gly Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn  
145 150 155 160  
Asp Val Val Glu Asp Phe Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu  
165 170 175  
Asp Lys Ile Ser Asp Val Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala  
180 185 190  
Leu Asn Ile Ser Asn Ser Val Arg Arg Gly Asn Phe Thr Glu Ala Phe  
195 200 205  
Ala Val Thr Gly Val Thr Ile Leu Leu Glu Ala Phe Pro Glu Phe Thr  
210 215 220  
Ile Pro Ala Leu Gly Ala Phe Val Ile Tyr Ser Lys Val Gln Glu Arg  
225 230 235 240  
Asn Glu Ile Ile Lys Thr Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys  
245 250 255  
Arg Trp Lys Asp Ser Tyr Glu Trp Met Met Gly Thr Trp Leu Ser Arg  
260 265 270  
Ile Ile Thr Gln Phe Asn Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu  
275 280 285  
Asn Tyr Gln Ala Gly Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys  
290 295 300  
Lys Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn

305	310	315	320
Leu Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile			
325	330	335	
Asn Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met			
340	345	350	
Leu Pro Lys Val Ile Asp Glu Leu Asn Glu Phe Asp Arg Asn Thr Lys			
355	360	365	
Ala Lys Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly			
370	375	380	
Glu Val Asp Lys Leu Lys Ala Lys Val Asn Asn Ser Phe Gln Asn			
385	390	395	

<210> 25  
<211> 1161  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<221> CDS  
<222> (1) ... (1158)

<400> 25			
atg gcc aac tcc cgt gac gac tcc acc tgc atc aag gtc aag aac aac			48
Met Ala Asn Ser Arg Asp Asp Ser Thr Cys Ile Lys Val Lys Asn Asn			
1	5	10	15

aga ctg cca tac gtt gcc gac aag gac tcc atc tcc cag gag atc ttc			96
Arg Leu Pro Tyr Val Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe			
20	25	30	

gag aac aag atc atc acc gac gag acc aac gtt caa aac tac tcc gac			144
Glu Asn Lys Ile Ile Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp			
35	40	45	

aag ttc tct ttg gac gag tcc atc ctg gac ggt cag gtc cca atc aac			192
Lys Phe Ser Leu Asp Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn			
50	55	60	

cca gag atc gtc gac cca ctg ttg cca aac gtc aac atg gag cca ttg			240
Pro Glu Ile Val Asp Pro Leu Leu Pro Asn Val Asn Met Glu Pro Leu			
65	70	75	80

aac ttg cca ggt gag gag atc gtc ttc tac gac gac atc acc aag tac			288
Asn Leu Pro Gly Glu Glu Ile Val Phe Tyr Asp Asp Ile Thr Lys Tyr			
85	90	95	

gtc gac tac ttg aac tcc tac tac tac ttg gag tct caa aag ttg tct			336
Val Asp Tyr Leu Asn Ser Tyr Tyr Leu Glu Ser Gln Lys Leu Ser			
100	105	110	

aac aac gtc gag aac atc acc ttg acc acc tcc gtc gag gag gcc ttg			384
Asn Asn Val Glu Asn Ile Thr Leu Thr Ser Val Glu Glu Ala Leu			
115	120	125	

ggt tac tct aac aag atc tac acc ttc ctg cca tcc ttg gct gag aag		432	
Gly Tyr Ser Asn Lys Ile Tyr Thr Phe Leu Pro Ser Leu Ala Glu Lys			
130	135	140	
gtt aac aag ggt gtt caa gct ggt ttg ttc ctg aac tgg gcc aac gag		480	
Val Asn Lys Gly Val Gln Ala Gly Leu Phe Leu Asn Trp Ala Asn Glu			
145	150	155	160
gtc gtc gag gac ttc acc acc aac atc atg aag aag gac acc ctg gac		528	
Val Val Glu Asp Phe Thr Thr Asn Ile Met Lys Lys Asp Thr Leu Asp			
165	170	175	
aag atc tcc gac gtc tcc gtc atc atc cca tac atc ggt cca gcc ttg		576	
Lys Ile Ser Asp Val Ser Val Ile Ile Pro Tyr Ile Gly Pro Ala Leu			
180	185	190	
aac atc ggt aac tcc gcc ctg aga ggt aac ttc aac cag gcc ttc gcc		624	
Asn Ile Gly Asn Ser Ala Leu Arg Gly Asn Phe Asn Gln Ala Phe Ala			
195	200	205	
acc gcc ggt gtc gcc ttc ctg ctg gag ggt ttc cca gag ttc acc atc		672	
Thr Ala Gly Val Ala Phe Leu Leu Glu Gly Phe Pro Glu Phe Thr Ile			
210	215	220	
cca gcc ctg ggt gtc ttc acc ttc tac tcc tcc atc cag gag aga gag		720	
Pro Ala Leu Gly Val Phe Thr Phe Tyr Ser Ser Ile Gln Glu Arg Glu			
225	230	235	240
aag atc atc aag acc atc gag aac tgc ttg gag cag aga gtc aag aga		768	
Lys Ile Ile Lys Thr Ile Glu Asn Cys Leu Glu Gln Arg Val Lys Arg			
245	250	255	
tgg aag gac tcc tac cag tgg atg gtt tcc aac tgg ctg tcc aga atc		816	
Trp Lys Asp Ser Tyr Gln Trp Met Val Ser Asn Trp Leu Ser Arg Ile			
260	265	270	
acc acc caa ttc aac cac atc aac tac cag atg tac gac tcc ctg tcc		864	
Thr Thr Gln Phe Asn His Ile Asn Tyr Gln Met Tyr Asp Ser Leu Ser			
275	280	285	
tac cag gcc gac gcc atc aag gcc aag atc gac ctg gag tac aag aag		912	
Tyr Gln Ala Asp Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys			
290	295	300	
tac tcc ggt tcc gac aag gag aac atc aag tcc cag gtc gag aac ctg		960	
Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu			
305	310	315	320
aag aac tcc ttg gac gtc aag atc tcc gag gcc atg aac aac atc aac		1008	
Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn			
325	330	335	
aag ttc atc cgt gag tgt tcc gtc acc tac ctg ttc aag aac atg ctg		1056	
Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu			
340	345	350	
cca aag gtc atc gac gag ctg aac aag ttc gac ctg aga acc aag acc		1104	

Pro Lys Val Ile Asp Glu Leu Asn Lys Phe Asp Leu Arg Thr Lys Thr			
355	360	365	
gag ctg atc aac ctg atc gac tcc cac aac atc atc ctg gtt ggt gag 1152			
Glu Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu			
370	375	380	
gtt gac taa 1161			
Val Asp			
385			
<210> 26			
<211> 386			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> Synthetic Construct			
<400> 26			
Met Ala Asn Ser Arg Asp Asp Ser Thr Cys Ile Lys Val Lys Asn Asn			
1	5	10	15
Arg Leu Pro Tyr Val Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe			
20	25	30	
Glu Asn Lys Ile Ile Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp			
35	40	45	
Lys Phe Ser Leu Asp Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn			
50	55	60	
Pro Glu Ile Val Asp Pro Leu Leu Pro Asn Val Asn Met Glu Pro Leu			
65	70	75	80
Asn Leu Pro Gly Glu Glu Ile Val Phe Tyr Asp Asp Ile Thr Lys Tyr			
85	90	95	
Val Asp Tyr Leu Asn Ser Tyr Tyr Leu Glu Ser Gln Lys Leu Ser			
100	105	110	
Asn Asn Val Glu Asn Ile Thr Leu Thr Thr Ser Val Glu Glu Ala Leu			
115	120	125	
Gly Tyr Ser Asn Lys Ile Tyr Thr Phe Leu Pro Ser Leu Ala Glu Lys			
130	135	140	
Val Asn Lys Gly Val Gln Ala Gly Leu Phe Leu Asn Trp Ala Asn Glu			
145	150	155	160
Val Val Glu Asp Phe Thr Thr Asn Ile Met Lys Lys Asp Thr Leu Asp			
165	170	175	
Lys Ile Ser Asp Val Ser Val Ile Ile Pro Tyr Ile Gly Pro Ala Leu			
180	185	190	
Asn Ile Gly Asn Ser Ala Leu Arg Gly Asn Phe Asn Gln Ala Phe Ala			
195	200	205	
Thr Ala Gly Val Ala Phe Leu Leu Glu Gly Phe Pro Glu Phe Thr Ile			
210	215	220	
Pro Ala Leu Gly Val Phe Thr Phe Tyr Ser Ser Ile Gln Glu Arg Glu			
225	230	235	240
Lys Ile Ile Lys Thr Ile Glu Asn Cys Leu Glu Gln Arg Val Lys Arg			
245	250	255	
Trp Lys Asp Ser Tyr Gln Trp Met Val Ser Asn Trp Leu Ser Arg Ile			
260	265	270	
Thr Thr Gln Phe Asn His Ile Asn Tyr Gln Met Tyr Asp Ser Leu Ser			
275	280	285	

Tyr Gln Ala Asp Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys  
 290                    295                    300  
 Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu  
 305                    310                    315                    320  
 Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn  
 325                    330                    335  
 Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu  
 340                    345                    350  
 Pro Lys Val Ile Asp Glu Leu Asn Lys Phe Asp Leu Arg Thr Lys Thr  
 355                    360                    365  
 Glu Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu  
 370                    375                    380  
 Val Asp  
 385

<210> 27  
 <211> 1149  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<221> CDS  
 <222> (1) ... (1146)

<400> 27  
 atg tcc atc tgc atc gag atc aac aac ggt gag ctg ttc ttc gtg gct      48  
 Met Ser Ile Cys Ile Glu Ile Asn Asn Gly Glu Leu Phe Phe Val Ala  
 1                    5                    10                    15

tcc gag aac agt tac aac gat gac aac atc aac act cct aag gag att      96  
 Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile Asn Thr Pro Lys Glu Ile  
 20                    25                    30

gac gac acc gtc act tct aac aac aac tac gaa aac gac ctg gac cag      144  
 Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr Glu Asn Asp Leu Asp Gln  
 35                    40                    45

gtc atc cta aac ttc aac tcc gag tcc gcc cct ggt ctg tcc gac gag      192  
 Val Ile Leu Asn Phe Asn Ser Glu Ser Ala Pro Gly Leu Ser Asp Glu  
 50                    55                    60

aag ctg aac ctg acc atc cag aac gac gct tac atc cca aag tac gac      240  
 Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala Tyr Ile Pro Lys Tyr Asp  
 65                    70                    75                    80

tcc aac ggt aca tcc gat atc gag cag cat gac gtt aac gag ctt aac      288  
 Ser Asn Gly Thr Ser Asp Ile Glu Gln His Asp Val Asn Glu Leu Asn  
 85                    90                    95

gtc ttc ttc tac tta gac gct cag aag gtg ccc gag ggt gag aac aac      336  
 Val Phe Phe Tyr Leu Asp Ala Gln Lys Val Pro Glu Gly Glu Asn Asn  
 100                    105                    110

gtc aat ctc acc tct tca att gac aca gcc ttg ttg gag cag cct aag      384

Val Asn Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu Gln Pro Lys			
115	120	125	
atc tac acc ttc ttc tcc tcc gag ttc atc aac aac gtc aac aag cct			432
Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile Asn Asn Val Asn Lys Pro			
130	135	140	
gtg cag gcc gca ttg ttc gta agc tgg att cag cag gtg tta gta gac			480
Val Gln Ala Ala Leu Phe Val Ser Trp Ile Gln Gln Val Leu Val Asp			
145	150	155	160
ttc act act gag gct aac cag aag tcc act gtt gac aag atc gct gac			528
Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr Val Asp Lys Ile Ala Asp			
165	170	175	
atc tcc atc gtc gtc cca tac atc ggt ctg gct ctg aac atc ggc aac			576
Ile Ser Ile Val Val Pro Tyr Ile Gly Leu Ala Leu Asn Ile Gly Asn			
180	185	190	
gag gca cag aag ggc aac ttc aag gat gcc ctt gag ttg ttg ggt gcc			624
Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala Leu Glu Leu Leu Gly Ala			
195	200	205	
ggt att ttg ttg gag ttc gaa ccc gag ctg ctg atc cct acc atc ctg			672
Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu Leu Ile Pro Thr Ile Leu			
210	215	220	
gtc ttc acg atc aag tcc ttc ctg ggt tcc tcc gac aac aag aac aag			720
Val Phe Thr Ile Lys Ser Phe Leu Gly Ser Ser Asp Asn Lys Asn Lys			
225	230	235	240
gtc att aag gcc atc aac aac gcc ctg aag gag cgt gac gag aag tgg			768
Val Ile Lys Ala Ile Asn Asn Ala Leu Lys Glu Arg Asp Glu Lys Trp			
245	250	255	
aag gaa gtc tat tcc ttc atc gtc tcg aac tgg atg acc aag atc aac			816
Lys Glu Val Tyr Ser Phe Ile Val Ser Asn Trp Met Thr Lys Ile Asn			
260	265	270	
acc cag ttc aac aag cga aag gag cag atg tac cag gct ctg cag aac			864
Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu Gln Asn			
275	280	285	
cag gtc aac gcc atc aag acc atc atc gag tcc aag tac aac tcc tac			912
Gln Val Asn Ala Ile Lys Thr Ile Ile Glu Ser Lys Tyr Asn Ser Tyr			
290	295	300	
acc ctg gag gag aag aac gag ctt acc aac aag tac gat atc aag cag			960
Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn Lys Tyr Asp Ile Lys Gln			
305	310	315	320
atc gag aac gag ctg aac cag aag gtc tcc atc gcc atg aac aac atc			1008
Ile Glu Asn Glu Leu Asn Gln Lys Val Ser Ile Ala Met Asn Asn Ile			
325	330	335	
gac agg ttc ctg acc gag tcc tcc atc tcc tac ctg atg aag ctc atc			1056
Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys Leu Ile			

340

345

350

aac gag gtc aag atc aac aag ctg cga gag tac gac gag aat gtc aag 1104  
 Asn Glu Val Lys Ile Asn Lys Leu Arg Glu Tyr Asp Glu Asn Val Lys  
 355 360 365

acg tac ctg ctg aac tac atc atc cag cac gga tcc atc ctg 1146  
 Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His Gly Ser Ile Leu  
 370 375 380

taa 1149

<210> 28

<211> 382

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 28

Met	Ser	Ile	Cys	Ile	Glu	Ile	Asn	Asn	Gly	Glu	Leu	Phe	Phe	Val	Ala
1				5				10						15	
Ser	Glu	Asn	Ser	Tyr	Asn	Asp	Asp	Asn	Ile	Asn	Thr	Pro	Lys	Glu	Ile
				20				25					30		
Asp	Asp	Thr	Val	Thr	Ser	Asn	Asn	Tyr	Glu	Asn	Asp	Leu	Asp	Gln	
				35				40			45				
Val	Ile	Leu	Asn	Phe	Asn	Ser	Glu	Ser	Ala	Pro	Gly	Leu	Ser	Asp	Glu
				50				55			60				
Lys	Leu	Asn	Leu	Thr	Ile	Gln	Asn	Asp	Ala	Tyr	Ile	Pro	Lys	Tyr	Asp
				65				70			75			80	
Ser	Asn	Gly	Thr	Ser	Asp	Ile	Glu	Gln	His	Asp	Val	Asn	Glu	Leu	Asn
				85				90			95				
Val	Phe	Phe	Tyr	Leu	Asp	Ala	Gln	Lys	Val	Pro	Glu	Gly	Glu	Asn	Asn
				100				105				110			
Val	Asn	Leu	Thr	Ser	Ser	Ile	Asp	Thr	Ala	Leu	Glu	Gln	Pro	Lys	
				115				120			125				
Ile	Tyr	Thr	Phe	Phe	Ser	Ser	Glu	Phe	Ile	Asn	Asn	Val	Asn	Lys	Pro
				130				135			140				
Val	Gln	Ala	Ala	Leu	Phe	Val	Ser	Trp	Ile	Gln	Gln	Val	Leu	Val	Asp
	145				150					155			160		
Phe	Thr	Thr	Glu	Ala	Asn	Gln	Lys	Ser	Thr	Val	Asp	Lys	Ile	Ala	Asp
				165					170			175			
Ile	Ser	Ile	Val	Val	Pro	Tyr	Ile	Gly	Leu	Ala	Leu	Asn	Ile	Gly	Asn
				180				185			190				
Glu	Ala	Gln	Lys	Gly	Asn	Phe	Lys	Asp	Ala	Leu	Glu	Leu	Leu	Gly	Ala
				195				200			205				
Gly	Ile	Leu	Leu	Glu	Phe	Glu	Pro	Glu	Leu	Leu	Ile	Pro	Thr	Ile	Leu
	210				215					220					
Val	Phe	Thr	Ile	Lys	Ser	Phe	Leu	Gly	Ser	Ser	Asp	Asn	Lys	Asn	Lys
	225			230					235			240			
Val	Ile	Lys	Ala	Ile	Asn	Asn	Ala	Leu	Lys	Glu	Arg	Asp	Glu	Lys	Trp
				245				250			255				
Lys	Glu	Val	Tyr	Ser	Phe	Ile	Val	Ser	Asn	Trp	Met	Thr	Lys	Ile	Asn
				260				265			270				
Thr	Gln	Phe	Asn	Lys	Arg	Lys	Glu	Gln	Met	Tyr	Gln	Ala	Leu	Gln	Asn
				275				280			285				

Gln	Val	Asn	Ala	Ile	Lys	Thr	Ile	Ile	Glu	Ser	Lys	Tyr	Asn	Ser	Tyr
290					295						300				
Thr	Leu	Glu	Glu	Lys	Asn	Glu	Leu	Thr	Asn	Lys	Tyr	Asp	Ile	Lys	Gln
305					310				315					320	
Ile	Glu	Asn	Glu	Leu	Asn	Gln	Lys	Val	Ser	Ile	Ala	Met	Asn	Asn	Ile
					325				330				335		
Asp	Arg	Phe	Leu	Thr	Glu	Ser	Ser	Ile	Ser	Tyr	Leu	Met	Lys	Leu	Ile
					340				345			350			
Asn	Glu	Val	Lys	Ile	Asn	Lys	Leu	Arg	Glu	Tyr	Asp	Glu	Asn	Val	Lys
					355				360			365			
Thr	Tyr	Leu	Leu	Asn	Tyr	Ile	Ile	Gln	His	Gly	Ser	Ile	Leu		
					370				375			380			

<210> 29  
<211> 1227  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<221> CDS  
<222> (1)....(1224)

<400> 29																
atg	gcc	cca	cca	cgt	ctg	tgt	att	aga	gtc	aac	aac	tca	gaa	tta	ttc	48
Met	Ala	Pro	Pro	Arg	Leu	Cys	Ile	Arg	Val	Asn	Asn	Ser	Glu	Leu	Phe	
1					5				10					15		
ttt gtc gct tcc gag tca agc tac aac gag aac gat att aac aca cct																
Phe	Val	Ala	Ser	Glu	Ser	Ser	Tyr	Asn	Glu	Asn	Asp	Ile	Asn	Thr	Pro	96
					20				25				30			
aaa gag att gac gat act acc aac cta aac aac aac tac cgg aac aac																
Lys	Glu	Ile	Asp	Asp	Thr	Thr	Asn	Leu	Asn	Asn	Tyr	Arg	Asn	Asn		144
					35				40			45				
ttg gat gag gtt att ttg gat tac aac tca cag acc atc cct caa att																
Leu	Asp	Glu	Val	Ile	Leu	Asp	Tyr	Asn	Ser	Gln	Thr	Ile	Pro	Gln	Ile	192
					50				55			60				
tcc aac cgt acc tta aac act ctt gtc caa gac aac tcc tac gtt cca																
Ser	Asn	Arg	Thr	Leu	Asn	Thr	Leu	Val	Gln	Asp	Asn	Ser	Tyr	Val	Pro	240
					65				70			75			80	
aga tac gat tct aac ggt acc tca gag atc gag gag tat gat gtt gtt																
Arg	Tyr	Asp	Ser	Asn	Gly	Thr	Ser	Glu	Ile	Glu	Glu	Tyr	Asp	Val	Val	288
					85				90			95				
gac ttt aac gtc ttt ttc tat ttg cat gcc cag aag gtg cca gaa ggt																
Asp	Phe	Asn	Val	Phe	Phe	Tyr	Leu	His	Ala	Gln	Lys	Val	Pro	Glu	Gly	336
					100				105			110				
gaa acc aac atc tca ttg act tct tcc att gat acc gcc ttg ttg gaa																
Glu	Thr	Asn	Ile	Ser	Leu	Thr	Ser	Ser	Ile	Asp	Thr	Ala	Leu	Leu	Glu	384
					115				120			125				

gag tcc aag gat atc ttc ttt tct tcg gag ttt atc gat act atc aac		432
Glu Ser Lys Asp Ile Phe Phe Ser Ser Glu Phe Ile Asp Thr Ile Asn		
130	135	140
aag cct gtc aac gcc gct ctg ttc att gat tgg att agc aag gtc atc		480
Lys Pro Val Asn Ala Ala Leu Phe Ile Asp Trp Ile Ser Lys Val Ile		
145	150	155
160		
aga gat ttt acc act gaa gct act caa aag tcc act gtt gat aag att		528
Arg Asp Phe Thr Thr Glu Ala Thr Gln Lys Ser Thr Val Asp Lys Ile		
165	170	175
gct gac atc tct ttg att gtc ccc tat gtc ggt ctt gct ttg aac atc		576
Ala Asp Ile Ser Leu Ile Val Pro Tyr Val Gly Leu Ala Leu Asn Ile		
180	185	190
att att gag gca gaa aag ggt aac ttt gag gag gct ttt gaa ttg ttg		624
Ile Ile Glu Ala Glu Lys Gly Asn Phe Glu Glu Ala Phe Glu Leu Leu		
195	200	205
gga gtt ggt att ttg ttg gag ttt gtt cca gaa ctt acc att cct gtc		672
Gly Val Gly Ile Leu Leu Glu Phe Val Pro Glu Leu Thr Ile Pro Val		
210	215	220
att tta gtt ttt acg atc aag tcc tac atc gat tca tac gag aac aag		720
Ile Leu Val Phe Thr Ile Lys Ser Tyr Ile Asp Ser Tyr Glu Asn Lys		
225	230	235
240		
aat aaa gca att aaa gct att aac aac tcc ttg atc gaa aga gag gct		768
Asn Lys Ala Ile Lys Ala Ile Asn Asn Ser Leu Ile Glu Arg Glu Ala		
245	250	255
aag tgg aag gaa atc tac tca tgg att gta tca aac tgg ctt act aga		816
Lys Trp Lys Glu Ile Tyr Ser Trp Ile Val Ser Asn Trp Leu Thr Arg		
260	265	270
att aac actcaa ttt aac aag aga aag gag caa atg tac cag gct ctg		864
Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu		
275	280	285
caa aac caa gtc gat gct atc aag act gca att gaa tac aag tac aac		912
Gln Asn Gln Val Asp Ala Ile Lys Thr Ala Ile Glu Tyr Lys Tyr Asn		
290	295	300
aac tat act tcc gat gag aag aac aga ctt gaa tct gaa tac aat atc		960
Asn Tyr Thr Ser Asp Glu Lys Asn Arg Leu Glu Ser Glu Tyr Asn Ile		
305	310	315
320		
aac aac att gaa gaa gag ttg aac aag aaa gtt tct ttg gct atg aag		1008
Asn Asn Ile Glu Glu Leu Asn Lys Lys Val Ser Leu Ala Met Lys		
325	330	335
aat atc gaa aga ttt atg acc gaa tcc tct atc tct tac ttg atg aag		1056
Asn Ile Glu Arg Phe Met Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys		
340	345	350

ttg atc aat gag gcc aag ggt aag ttg aag aag tac gat aac cac		1104
Leu Ile Asn Glu Ala Lys Val Gly Lys Leu Lys Tyr Asp Asn His		
355	360	365
gtt aag agc gat ctg ctg aac tac att ctc gac cac aga tca atc ctg		1152
Val Lys Ser Asp Leu Leu Asn Tyr Ile Leu Asp His Arg Ser Ile Leu		
370	375	380
gga gag cag aca aac gag ctg agt gat ttg gtt act tcc act ttg aac		1200
Gly Glu Gln Thr Asn Glu Leu Ser Asp Leu Val Thr Ser Thr Leu Asn		
385	390	395
tcc tcc att cca ttt gag ctt tct taa		1227
Ser Ser Ile Pro Phe Glu Leu Ser		
405		

<210> 30  
<211> 408  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 30			
Met Ala Pro Pro Arg Leu Cys Ile Arg Val Asn Asn Ser Glu Leu Phe			
1	5	10	15
Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu Asn Asp Ile Asn Thr Pro			
20	25	30	
Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn Asn Tyr Arg Asn Asn			
35	40	45	
Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser Gln Thr Ile Pro Gln Ile			
50	55	60	
Ser Asn Arg Thr Leu Asn Thr Leu Val Gln Asp Asn Ser Tyr Val Pro			
65	70	75	80
Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile Glu Glu Tyr Asp Val Val			
85	90	95	
Asp Phe Asn Val Phe Phe Tyr Leu His Ala Gln Lys Val Pro Glu Gly			
100	105	110	
Glu Thr Asn Ile Ser Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu			
115	120	125	
Glu Ser Lys Asp Ile Phe Phe Ser Ser Glu Phe Ile Asp Thr Ile Asn			
130	135	140	
Lys Pro Val Asn Ala Ala Leu Phe Ile Asp Trp Ile Ser Lys Val Ile			
145	150	155	160
Arg Asp Phe Thr Thr Glu Ala Thr Gln Lys Ser Thr Val Asp Lys Ile			
165	170	175	
Ala Asp Ile Ser Leu Ile Val Pro Tyr Val Gly Leu Ala Leu Asn Ile			
180	185	190	
Ile Ile Glu Ala Glu Lys Gly Asn Phe Glu Glu Ala Phe Glu Leu Leu			
195	200	205	
Gly Val Gly Ile Leu Leu Glu Phe Val Pro Glu Leu Thr Ile Pro Val			
210	215	220	
Ile Leu Val Phe Thr Ile Lys Ser Tyr Ile Asp Ser Tyr Glu Asn Lys			
225	230	235	240
Asn Lys Ala Ile Lys Ala Ile Asn Asn Ser Leu Ile Glu Arg Glu Ala			

245.	250	255
Lys Trp Lys Glu Ile Tyr Ser Trp Ile Val Ser Asn Trp Leu Thr Arg		
260	265	270
Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu		
275	280	285
Gln Asn Gln Val Asp Ala Ile Lys Thr Ala Ile Glu Tyr Lys Tyr Asn		
290	295	300
Asn Tyr Thr Ser Asp Glu Lys Asn Arg Leu Glu Ser Glu Tyr Asn Ile		
305	310	315
Asn Asn Ile Glu Glu Leu Asn Lys Lys Val Ser Leu Ala Met Lys		
325	330	335
Asn Ile Glu Arg Phe Met Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys		
340	345	350
Leu Ile Asn Glu Ala Lys Val Gly Lys Leu Lys Lys Tyr Asp Asn His		
355	360	365
Val Lys Ser Asp Leu Leu Asn Tyr Ile Leu Asp His Arg Ser Ile Leu		
370	375	380
Gly Glu Gln Thr Asn Glu Leu Ser Asp Leu Val Thr Ser Thr Leu Asn		
385	390	395
Ser Ser Ile Pro Phe Glu Leu Ser		400
405		

<210> 31  
<211> 1233  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<221> CDS  
<222> (1) ... (1230)

<400> 31  
atg gcc aaa aat acc ggt aaa tct gaa cag tgt att att gtt aat aat 48  
Met Ala Lys Asn Thr Gly Lys Ser Glu Gln Cys Ile Ile Val Asn Asn  
1 5 10 15

gag gat tta ttt ttc ata gct aat aaa gat agt ttt tca aaa gat tta 96  
Glu Asp Leu Phe Phe Ile Ala Asn Lys Asp Ser Phe Ser Lys Asp Leu  
20 25 30

gct aaa gca gaa act ata gca tat aat aca caa aat aat act ata gaa 144  
Ala Lys Ala Glu Thr Ile Ala Tyr Asn Thr Gln Asn Asn Thr Ile Glu  
35 40 45

aat aat ttt tct ata gat cag ttg att tta gat aat gat tta agc agt 192  
Asn Asn Phe Ser Ile Asp Gln Leu Ile Leu Asp Asn Asp Leu Ser Ser  
50 55 60

ggc ata gac tta cca aat gaa aac aca gaa cca ttt aca aat ttt gac 240  
Gly Ile Asp Leu Pro Asn Glu Asn Thr Glu Pro Phe Thr Asn Phe Asp  
65 70 75 80

gac ata gat atc cct gtg tat att aaa caa tct gct tta aaa aaa att 288  
Asp Ile Asp Ile Pro Val Tyr Ile Lys Gln Ser Ala Leu Lys Ile

85

90

95

ttt gtg gat gga gat agc ctt ttt gaa tat tta cat gct caa aca aca	100	105	110	336
Phe Val Asp Gly Asp Ser Leu Phe Glu Tyr Leu His Ala Gln Thr Phe				
cct tct aat ata gaa aat cta caa cta acg aat tca tta aat gat gct	115	120	125	384
Pro Ser Asn Ile Glu Asn Leu Gln Leu Thr Asn Ser Leu Asn Asp Ala				
tta aga aat aat aat aaa gtc tat act ttt ttt tct aca aac ctt gtt	130	135	140	432
Leu Arg Asn Asn Lys Val Tyr Thr Phe Ser Thr Asn Leu Val				
gaa aaa gct aat aca gtt gta ggt gct tca ctt ttt gta aac tgg gta	145	150	155	480
Glu Lys Ala Asn Thr Val Val Gly Ala Ser Leu Phe Val Asn Trp Val				
aaa gga gta ata gat gat ttt aca tct gaa tcc aca caa aaa agt act	165	170	175	528
Lys Gly Val Ile Asp Asp Phe Thr Ser Glu Ser Thr Gln Lys Ser Thr				
ata gat aaa gtt tca gat gta tcc ata att att ccc tat ata gga cct	180	185	190	576
Ile Asp Lys Val Ser Asp Val Ser Ile Ile Ile Pro Tyr Ile Gly Pro				
gct ttg aat gta gga aat gaa aca gct aaa gaa aat ttt aaa aat gct	195	200	205	624
Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Glu Asn Phe Lys Asn Ala				
ttt gaa ata ggt gga gcc gct atc tta atg gag ttt att cca gaa ctt	210	215	220	672
Phe Glu Ile Gly Gly Ala Ala Leu Met Glu Phe Ile Pro Glu Leu				
att gta cct ata gtt gga ttt ttt aca tta gaa tca tat gta gga aat	225	230	235	720
Ile Val Pro Ile Val Gly Phe Phe Thr Leu Glu Ser Tyr Val Gly Asn				
aaa ggg cat att att atg acg ata tcc aat gct tta aag aaa agg gat	245	250	255	768
Lys Gly His Ile Ile Met Thr Ile Ser Asn Ala Leu Lys Lys Arg Asp				
caa aaa tgg aca gat atg tat ggt ttg ata gta tcg cag tgg ctc tca	260	265	270	816
Gln Lys Trp Thr Asp Met Tyr Gly Leu Ile Val Ser Gln Trp Leu Ser				
acg gtt aat act caa ttt tat aca ata aaa gaa aga atg tac aat gct	275	280	285	864
Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Arg Met Tyr Asn Ala				
tta aat aat caa tca caa gca ata gaa aaa ata ata gaa gat caa tat	290	295	300	912
Leu Asn Asn Gln Ser Gln Ala Ile Glu Lys Ile Ile Glu Asp Gln Tyr				
aat aga tat agt gaa gaa gat aaa atg aat att aac att gat ttt aat	305	310	315	960
Asn Arg Tyr Ser Glu Glu Asp Lys Met Asn Ile Asn Ile Asp Phe Asn				

gat ata gat ttt aaa ctt aat caa agt ata aat tta gca ata aac aat Asp Ile Asp Phe Lys Leu Asn Gln Ser Ile Asn Leu Ala Ile Asn Asn 325 330 335	1008
ata gat gat ttt ata aac caa tgt tct ata tca tat cta atg aat aga Ile Asp Asp Phe Ile Asn Gln Cys Ser Ile Ser Tyr Leu Met Asn Arg 340 345 350	1056
atg att cca tta gct gta aaa aag tta aaa gac ttt gat gat aat ctt Met Ile Pro Leu Ala Val Lys Lys Leu Lys Asp Phe Asp Asp Asn Leu 355 360 365	1104
aag aga gat tta ttg gag tat ata gat aca aat gaa cta tat tta ctt Lys Arg Asp Leu Leu Glu Tyr Ile Asp Thr Asn Glu Leu Tyr Leu Leu 370 375 380	1152
gat gaa gta aat att cta aaa tca aaa gta aat aga cac cta aaa gac Asp Glu Val Asn Ile Leu Lys Ser Lys Val Asn Arg His Leu Lys Asp 385 390 395 400	1200
agt ata cca ttt gat ctt tca cta tat acc taa Ser Ile Pro Phe Asp Leu Ser Leu Tyr Thr 405 410	1233

<210> 32  
<211> 410  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

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<400> 32
Met Ala Lys Asn Thr Gly Lys Ser Glu Gln Cys Ile Ile Val Asn Asn
      1          5          10          15
Glu Asp Leu Phe Phe Ile Ala Asn Lys Asp Ser Phe Ser Lys Asp Leu
      20         25         30
Ala Lys Ala Glu Thr Ile Ala Tyr Asn Thr Gln Asn Asn Thr Ile Glu
      35         40         45
Asn Asn Phe Ser Ile Asp Gln Leu Ile Leu Asp Asn Asp Leu Ser Ser
      50         55         60
Gly Ile Asp Leu Pro Asn Glu Asn Thr Glu Pro Phe Thr Asn Phe Asp
      65         70         75         80
Asp Ile Asp Ile Pro Val Tyr Ile Lys Gln Ser Ala Leu Lys Lys Ile
      85         90         95
Phe Val Asp Gly Asp Ser Leu Phe Glu Tyr Leu His Ala Gln Thr Phe
      100        105        110
Pro Ser Asn Ile Glu Asn Leu Gln Leu Thr Asn Ser Leu Asn Asp Ala
      115        120        125
Leu Arg Asn Asn Asn Lys Val Tyr Thr Phe Phe Ser Thr Asn Leu Val
      130        135        140
Glu Lys Ala Asn Thr Val Val Gly Ala Ser Leu Phe Val Asn Trp Val
      145        150        155        160
Lys Gly Val Ile Asp Asp Phe Thr Ser Glu Ser Thr Gln Lys Ser Thr
      165        170        175

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Ile Asp Lys Val Ser Asp Val Ser Ile Ile Pro Tyr Ile Gly Pro  
     180                  185                  190  
 Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Glu Asn Phe Lys Asn Ala  
     195                  200                  205  
 Phe Glu Ile Gly Gly Ala Ala Ile Leu Met Glu Phe Ile Pro Glu Leu  
     210                  215                  220  
 Ile Val Pro Ile Val Gly Phe Phe Thr Leu Glu Ser Tyr Val Gly Asn  
     225                  230                  235                  240  
 Lys Gly His Ile Ile Met Thr Ile Ser Asn Ala Leu Lys Lys Arg Asp  
     245                  250                  255  
 Gln Lys Trp Thr Asp Met Tyr Gly Leu Ile Val Ser Gln Trp Leu Ser  
     260                  265                  270  
 Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Arg Met Tyr Asn Ala  
     275                  280                  285  
 Leu Asn Asn Gln Ser Gln Ala Ile Glu Lys Ile Ile Glu Asp Gln Tyr  
     290                  295                  300  
 Asn Arg Tyr Ser Glu Glu Asp Lys Met Asn Ile Asn Ile Asp Phe Asn  
     305                  310                  315                  320  
 Asp Ile Asp Phe Lys Leu Asn Gln Ser Ile Asn Leu Ala Ile Asn Asn  
     325                  330                  335  
 Ile Asp Asp Phe Ile Asn Gln Cys Ser Ile Ser Tyr Leu Met Asn Arg  
     340                  345                  350  
 Met Ile Pro Leu Ala Val Lys Lys Leu Lys Asp Phe Asp Asp Asn Leu  
     355                  360                  365  
 Lys Arg Asp Leu Leu Glu Tyr Ile Asp Thr Asn Glu Leu Tyr Leu Leu  
     370                  375                  380  
 Asp Glu Val Asn Ile Leu Lys Ser Lys Val Asn Arg His Leu Lys Asp  
     385                  390                  395                  400  
 Ser Ile Pro Phe Asp Leu Ser Leu Tyr Thr  
     405                  410

<210> 33  
 <211> 1314  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<221> CDS  
 <222> (10)...(1305)

<400> 33  
 gaattcacg atg tct tac act aac gac aaa atc ctg atc ctg tac ttc aac 51  
 Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn  
     1                  5                  10

aaa ctg tac aaa aaa atc aaa gac aac tct atc ctg gac atg cgt tac 99  
 Lys Leu Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr  
     15                  20                  25                  30

gaa aac aac aaa ttc atc gac atc tct ggc tat ggt tct aac atc tct 147  
 Glu Asn Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser  
     35                  40                  45

atc aac ggt gac gtc tac atc tac tct act aac cgc aac cag ttc ggt 195

Ile Asn Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly			
50	55	60	
atc tac tct tct aaa ccg tct gaa gta aac atc gct cag aac aac gac			243
Ile Tyr Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp			
65	70	75	
atc atc tac aac ggt cgt tac cag aac ttc tct atc tct ttc tgg gtt			291
Ile Ile Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val			
80	85	90	
cgt atc ccg aaa tac ttc aac aaa gtt aac ctg aac aac gaa tac act			339
Arg Ile Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr			
95	100	105	110
atc atc gac tgc atc cgt aac aac aac tct ggt tgg aaa atc tct ctg			387
Ile Ile Asp Cys Ile Arg Asn Asn Ser Gly Trp Lys Ile Ser Leu			
115	120	125	
aac tac aac aaa atc atc tgg act ctg cag gac act gct ggt aac aac			435
Asn Tyr Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn			
130	135	140	
cag aaa ctg gtt ttc aac tac act cag atg atc tct atc tct gac tac			483
Gln Lys Leu Val Phe Asn Tyr Gln Met Ile Ser Ile Ser Asp Tyr			
145	150	155	
att aat aaa tgg.atc ttc gtt act atc act aac aac cgt ctg ggt aac			531
Ile Asn Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn			
160	165	170	
tct cgt atc tac atc aac ggt aac ctg atc gat gaa aaa tct atc tct			579
Ser Arg Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser			
175	180	185	190
aac ctg ggt gac atc cac gtt tct gac aac atc ctg ttc aaa atc gtt			627
Asn Leu Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val			
195	200	205	
ggt tgc aac gac acg cgt tac gtt ggt atc cgt tac ttc aaa gtt ttc			675
Gly Cys Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe			
210	215	220	
gac act gaa ctg ggt aaa act gaa atc gaa act ctg tac tct gac gaa			723
Asp Thr Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu			
225	230	235	
ccg gac ccg tct atc ctg aaa gac ttc tgg ggt aac tac ctg ctg tac			771
Pro Asp Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr			
240	245	250	
aac aaa cgt tac tac ctg ctg aac ctg ctc cgg act gac aaa tct atc			819
Asn Lys Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile			
255	260	265	270
act cag aac tct aac ttc ctg aac atc aac cag cag cgt ggt gtt tat			867
Thr Gln Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr			

275

280

285

cag aaa cct aat atc ttc tct aac act cgt ctg tac act ggt gtt gaa Gln Lys Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu 290	295	300	915	
gtt atc atc cgt aaa aac ggt tct act gac atc tct aac act gac aac Val Ile Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn 305	310	315	963	
ttc gta cgt aaa aac gac ctg gct tac atc aac gtt gac cgt gac Phe Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp 320	325	330	1011	
gtt gaa tac cgt ctg tac gct gac atc tct atc gct aaa ccg gaa aaa Val Glu Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys 335	340	345	350	1059
atc atc aaa ctg atc cgt act tct aac tct aac aac tct ctg ggt cag Ile Ile Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln 355	360	365	1107	
atc atc gtt atg gac tcg atc ggt aac aac tgc act atg aac ttc cag Ile Ile Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln 370	375	380	1155	
aac aac aac ggt ggt aac atc ggt ctg ctg ggt ttc cac tct aac aac Asn Asn Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn 385	390	395	1203	
ctg gtt gct tct tca tgg tac tac aac aac atc cgt aaa aac act tct Leu Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser 400	405	410	1251	
tct aac ggt tgc ttc tgg tct ttc atc tct aaa gaa cac ggt tgg cag Ser Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln 415	420	425	430	1299
gaa aac taagaattc Glu Asn			1314	

<210> 34  
<211> 432  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 34  
Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu  
1 5 10 15  
Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn  
20 25 30  
Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn

35	40	45
Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr		
50	55	60
Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile		
65	70	75
Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile		
85	90	95
Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile		
100	105	110
Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr		
115	120	125
Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys		
130	135	140
Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn		
145	150	155
160		
Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg		
165	170	175
Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu		
180	185	190
Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys		
195	200	205
Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr		
210	215	220
Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp		
225	230	235
240		
Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys		
245	250	255
Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln		
260	265	270
Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys		
275	280	285
Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile		
290	295	300
Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val		
305	310	315
320		
Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu		
325	330	335
Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile		
340	345	350
Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile		
355	360	365
Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn		
370	375	380
Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val		
385	390	395
400		
Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn		
405	410	415
Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn		
420	425	430